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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:17:19 ; Search time 19 Seconds
(without alignments)
16.303 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADWSA 6

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	236	4	US-09-632-570-17
2	37	92.5	236	4	US-09-632-575-47
3	37	92.5	938	4	US-09-252-991A-23882
4	36	90.0	68	4	US-09-252-991A-18367
5	36	90.0	142	4	US-09-252-991A-31533
6	36	90.0	174	4	US-09-325-932A-163
7	36	90.0	225	4	US-09-325-932A-162
8	36	90.0	242	4	US-09-345-236B-3
9	36	90.0	378	4	US-09-325-932A-158
10	36	90.0	445	4	US-09-252-991A-22368
11	36	90.0	462	4	US-09-252-991A-21704
12	34	85.0	44	3	US-09-905-223-274
13	33	82.5	74	1	US-08-379-538-2
14	33	82.5	136	2	US-08-774-065-2
15	33	82.5	164	4	US-09-252-991A-23817
16	33	82.5	218	1	US-08-032-848C-10
17	33	82.5	218	1	US-08-438-870-10
18	33	82.5	218	2	US-08-169-948B-34
19	33	82.5	218	2	US-08-448-873-34
20	33	82.5	218	3	US-08-382-452D-34
21	33	82.5	218	3	US-09-216-295-1
22	33	82.5	218	4	US-08-507-362A-18
23	33	82.5	218	4	US-09-916-494A-34
24	33	82.5	218	4	US-09-632-570-1
25	33	82.5	218	4	US-09-632-575-31
26	33	82.5	232	3	US-09-146-770-1
27	33	82.5	232	4	US-09-633-084-1

28	33	82.5	232	4	US-10-075-872-1	Sequence 1, Appli
29	33	82.5	232	4	US-10-261-997-1	Sequence 9, Appli
30	33	82.5	234	1	US-08-032-848C-9	Sequence 9, Appli
31	33	82.5	234	1	US-08-438-870-9	Sequence 3, Appli
32	33	82.5	234	3	US-09-146-770-3	Sequence 4, Appli
33	33	82.5	234	3	US-09-216-295-3	Sequence 4, Appli
34	33	82.5	234	3	US-09-216-295-4	Sequence 4, Appli
35	33	82.5	234	3	US-09-633-084-3	Sequence 3, Appli
36	33	82.5	234	4	US-09-633-084-4	Sequence 3, Appli
37	33	82.5	234	4	US-10-075-872-3	Sequence 4, Appli
38	33	82.5	234	4	US-10-075-872-4	Sequence 3, Appli
39	33	82.5	234	4	US-10-261-997-3	Sequence 3, Appli
40	33	82.5	234	4	US-10-261-997-4	Sequence 3, Appli
41	33	82.5	234	4	US-09-632-570-3	Sequence 4, Appli
42	33	82.5	234	4	US-09-632-570-4	Sequence 3, Appli
43	33	82.5	234	4	US-09-632-575-33	Sequence 33, Appli
44	33	82.5	234	4	US-09-632-575-34	Sequence 34, Appli
45	33	82.5	234	4	US-09-632-570-15	Sequence 15, Appli
46	33	82.5	238	4	US-09-632-575-45	Sequence 45, Appli
47	33	82.5	238	4	US-09-216-295-15	Sequence 15, Appli
48	33	82.5	316	4	US-09-252-991A-17312	Sequence 17312, A
49	33	82.5	467	1	US-08-140-104A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-632-570-17
; Sequence 17, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-570-17

Query Match 92.5%; Score 37; DB 4; Length 236;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSA 6

Db 63 ADWSWS 68

RESULT 2
US-09-632-575-47

; Sequence 47, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-575-47

Query Match      92.5%; Score 37; DB 4; Length 236;
Best Local Similarity 83.3%; Pred. No. 89;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 3
US-09-252-991A-23882
; Sequence 23882, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23882
; LENGTH: 938
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23882

Query Match      92.5%; Score 37; DB 4; Length 938;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSWA 6
Db      581 ADMAWA 586

RESULT 4
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

Query Match      90.0%; Score 36; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
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Db      2 DWSWA 6

RESULT 5
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match      90.0%; Score 36; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      94 ADWSW 98

RESULT 6
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

Query Match      90.0%; Score 36; DB 4; Length 174;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
Db      109 ADWSW 113

RESULT 7
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
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FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325.932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 162
LENGTH: 225
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 100 ADMSW 104

RESULT 8
US-09-345-236B-3
Sequence 3, Application US/09345236B
Patent No. 6521454
GENERAL INFORMATION:
APPLICANT: Becnel, James J.
APPLICANT: Tuku, Fukuda
APPLICANT: Moser, Bettina
APPLICANT: Cockburn, Andrew
APPLICANT: White, Susan E.
APPLICANT: Undeen, Albert H.
TITLE OF INVENTION: No. 6521454el Baculoviruses, Insecticidal
TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
FILE REFERENCE: 21042.0004
CURRENT APPLICATION NUMBER: US/09/345.236B
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 148
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 242
TYPE: PRT
ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match 90.0%; Score 36; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 80 DMSWA 84

RESULT 9
US-09-325-932A-158
Sequence 158, Application US/09325932A
Patent No. 6451604
GENERAL INFORMATION:
APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant develop
FILE REFERENCE: 1022
CURRENT APPLICATION NUMBER: US/09/325.932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 158
LENGTH: 378
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 128 ADMSW 132

RESULT 10
US-09-252-991A-22368
Sequence 22368, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22368
LENGTH: 445
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

Query Match 90.0%; Score 36; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 304 DMSWA 308

RESULT 11
US-09-252-991A-21704
Sequence 21704, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252.991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21704
LENGTH: 462
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match 90.0%; Score 36; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 169 DMSWA 173

RESULT 12
US-08-905-223-274

; Sequence 274, Application US/08905223
; Patent No. 6220209
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelters, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 274:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -26...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 9.6
; OTHER INFORMATION: seq WLIALASWSWALC/RI
US-08-905-223-274

Query Match 85.0%; Score 34; DB 3; Length 44;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 19 ASWSWA 24
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RESULT 13
US-08-379-538-2
; Sequence 2, Application US/08379538
; Patent No. 5804554
; GENERAL INFORMATION:
; APPLICANT: Volkmann, Robert A.
; APPLICANT: Saccomano, Nicholas A.
; APPLICANT: Nason II, Deane M.
; APPLICANT: Heck, Steven D.
; APPLICANT: Ronau, Robert T.
; TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
; TITLE OF INVENTION: FROM FILISTATA HIBERNALIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc
; STREET: 235 East 42nd Street

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,538
; FILING DATE: 3-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/887073
; FILING DATE: 21-MAY-1992
; APPLICATION NUMBER: PCT/US93/03921
; FILING DATE: 30-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Zielinski, Bryan
; REGISTRATION NUMBER: 34,462
; REFERENCE/DOCKET NUMBER: PC8175A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 573-4585
; TELEFAX: (212) 573-1939
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: venom
US-08-379-538-2

Query Match 82.5%; Score 33; DB 1; Length 74;
Best Local Similarity 80.0%; Pred. No. 11e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 52 DWSWS 56
|||||

RESULT 14
US-08-774-065-2
; Sequence 2, Application US/08774065
; Patent No. 5989899
; GENERAL INFORMATION:
; APPLICANT: Bower, Benjamin
; APPLICANT: Clarkson, Kathleen
; APPLICANT: Larenas, Edmund
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: NOVEL OVERSIZED CELLULASE COMPOSITIONS
; TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND
; TITLE OF INVENTION: IN THE TREATMENT OF TEXTILES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL
; STREET: 925 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0


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; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032.848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-032-848C-10
;
Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0
;
Qy 1 ADWSWA 6
Db 46 ADWQWS 51
;
RESULT 17
US-08-438-870-10
; Sequence 10, Application US/08438870
; Patent No. 5753484
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of EG
; TITLE OF INVENTION: III Cellulase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,870
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 742-7555
TELEFAX: 415 742-7217
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |
Db 46 ADWQWS 51

RESULT 18
US-08-169-948B-34
Sequence 34, Application US/08169948B
Patent No. 5861271
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Katherine
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5861271e1 Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expression
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,948B
FILING DATE: DEC 17 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Horn, Margaret A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-169-948B-34

Query Match 82.5%; Score 33; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |
Db 46 ADWQWS 51

RESULT 19
US-08-448-873-34
Sequence 34, Application US/08448873
Patent No. 5874276
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Ward, Michael
APPLICANT: Clarkson, Kathleen
APPLICANT: Collier, Katherine A.
APPLICANT: Larenas, Edmund
TITLE OF INVENTION: No. 5874276e1 Cellulase Enzymes and Systems
TITLE OF INVENTION: For Their Expressions
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,873
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/169,948
FILING DATE: 17-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC226D14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-448-873-34

Query Match 82.5%; Score 33; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
||| |
Db 46 ADWQWS 51

RESULT 20
US-08-382-452D-34
Sequence 34, Application US/08382452D
Patent No. 6268196
GENERAL INFORMATION:
APPLICANT: Fowler, Timothy
APPLICANT: Clarkson, Kathleen A.
APPLICANT: Ward, Michael
APPLICANT: Collier, Katherine D.
APPLICANT: Larenas, Edmund A.
TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS
TITLE OF INVENTION: FOR THEIR EXPRESSION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/382,452D
; FILING DATE: February 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 36,696
; REFERENCE/DOCKET NUMBER: GC226-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-382-452D-34

Query Match 82.5%; Score 33; DB 3; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 46 ADWQWS 51

RESULT 21
US-09-216-295-1
; Sequence 1, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma longibrachiatum
; US-09-216-295-1

Query Match 82.5%; Score 33; DB 3; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 46 ADWQWS 51

RESULT 22
US-08-507-362A-18
; Sequence 18, Application US/08507362A
; Patent No. 6562340
; GENERAL INFORMATION:
; APPLICANT: Bedford, Michael
; Morgan, Andrew
; Fowler, Timothy
; Ward, Michael
; Clarkson, Kathleen
; Collier, Katherine
; Larenas, Edmund
; TITLE OF INVENTION: An Enzyme Feed Additive and Animal Feed Including It
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,362A
; FILING DATE: 27-Oct-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Castaneda, Janet
; REGISTRATION NUMBER: 33,228
; REFERENCE/DOCKET NUMBER: GC226-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 846-4072
; TELEFAX: (650) 845-6504
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-507-362A-18

Query Match 82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 46 ADWQWS 51

RESULT 23
US-09-916-494A-34
; Sequence 34, Application US/09916494A
; Patent No. 6620605
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Ward, Michael
; APPLICANT: Collier, Katherine D.
; APPLICANT: Larenas, Edmund
; TITLE OF INVENTION: Method and Compositions for Treating
; TITLE OF INVENTION: Cellulose Containing Fabrics Using Truncated Cellulase
; FILE REFERENCE: GC226-C4
; CURRENT APPLICATION NUMBER: US/09/916,494A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 08/382,452
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: US 08/169,948
; PRIOR FILING DATE: 1993-12-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
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; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma longibrachiatum
US-09-916-494A-34

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      46 ADWQWS 51

RESULT 24
US-09-632-570-1
; Sequence 1, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949a1 Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632.570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-570-1

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      46 ADWQWS 51

RESULT 25
US-09-632-575-31
; Sequence 31, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632.575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-575-31

Query Match      82.5%; Score 33; DB 4; Length 218;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      46 ADWQWS 51

RESULT 26
US-09-146-770-1
; Sequence 1, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/146,770
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-09-146-770-1

Query Match      82.5%; Score 33; DB 3; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      60 ADWQWS 65

RESULT 27
US-09-633-084-1
; Sequence 1, Application US/09633084
; Patent No. 6407046
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/633,084
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/146,770
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-09-633-084-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 ADWSWA 6
      |||||
Db      60 ADWQWS 65

RESULT 28
US-10-075-872-1
; Sequence 1, Application US/10075872
; Patent No. 6500211
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/075,872
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
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; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-10-075-872-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||
Db      60 ADMQWS 65

RESULT 29
US-10-261-997-1
; Sequence 1, Application US/10261997
; Patent No. 6582750
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/261,997
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 232
; TYPE: PRT
; ORGANISM: T. reesei
US-10-261-997-1

Query Match      82.5%; Score 33; DB 4; Length 232;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||
Db      60 ADMQWS 65

US-08-032-848C-9
; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-032-848C-9

Query Match      82.5%; Score 33; DB 1; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||
Db      62 ADMQWS 67

US-08-438-870-9
; Sequence 9, Application US/08438870
; Patent No. 5753484
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of EG
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,870
; FILING DATE: May 10, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Christopher L. Stone
; REGISTRATION NUMBER: 35,696
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7555
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-870-9

Query Match      82.5%; Score 33; DB 1; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||
Db      62 ADMQWS 67

US-08-032-848C-9
; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-032-848C-9

Query Match      82.5%; Score 33; DB 1; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
      |||||
Db      62 ADMQWS 67

US-08-438-870-9
; Sequence 9, Application US/08032848C
; Patent No. 5475101
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
```

```
RESULT 32
US-09-146-770-3
; Sequence 3, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT FILING DATE: 1998-09-03
; CURRENT APPLICATION NUMBER: US/09/146,770
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-09-146-770-3
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 33
US-09-146-770-4
; Sequence 4, Application US/09146770
; Patent No. 6187732
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT FILING DATE: 1998-09-03
; CURRENT APPLICATION NUMBER: US/09/146,770
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: H. schweinitzii
US-09-146-770-4
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 34
US-09-216-295-3
; Sequence 3, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; TITLE OF INVENTION: No. 6268328e1 Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-216-295-3
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 35
US-09-216-295-4
; Sequence 4, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; TITLE OF INVENTION: No. 6268328e1 Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Hypocrea schweinitzii
US-09-216-295-4
Query Match      82.5%; Score 33; DB 3; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 36
US-09-633-084-3
; Sequence 3, Application US/09633084
; Patent No. 6407046
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/633,084
; CURRENT FILING DATE: 2000-08-04
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-09-633-084-3
Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADWQWS 67

RESULT 37
US-09-633-084-4
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```
; Sequence 4, Application US/09633084
; Patent No. 6407046
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/09/633,084
; CURRENT FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 09/146,770
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: H. schweinitzii
US-09-633-084-4

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADQWMS 67

RESULT 38
US-10-075-872-3
; Sequence 3, Application US/10075872
; Patent No. 6500211
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/075,872
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-10-075-872-3

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADQWMS 67

RESULT 39
US-10-075-872-4
; Sequence 4, Application US/10075872
; Patent No. 6500211
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/075,872
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: H. schweinitzii

US-10-075-872-4

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADQWMS 67

RESULT 40
US-10-261-997-3
; Sequence 3, Application US/10261997
; Patent No. 6582750
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/261,997
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: T. reesei
US-10-261-997-3

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADQWMS 67

RESULT 41
US-10-261-997-4
; Sequence 4, Application US/10261997
; Patent No. 6582750
; GENERAL INFORMATION:
; APPLICANT: Fowler, Timothy
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC546
; CURRENT APPLICATION NUMBER: US/10/261,997
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: H. schweinitzii
US-10-261-997-4

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      62 ADQWMS 67

RESULT 42
US-09-632-570-3
; Sequence 3, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
```

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; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-570-3

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
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Db 62 ADWQWS 67

RESULT 43
US-09-632-570-4
; Sequence 4, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Hypocrea schweinitzii
US-09-632-570-4

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
   |||||
Db 62 ADWQWS 67

RESULT 44
US-09-632-575-33
; Sequence 33, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-09-632-575-33

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
   |||||
Db 62 ADWQWS 67

RESULT 45
US-09-632-575-34
; Sequence 34, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Hypocrea schweinitzii
US-09-632-575-34

Query Match      82.5%; Score 33; DB 4; Length 234;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
   |||||
Db 62 ADWQWS 67

RESULT 46
US-09-632-570-15
; Sequence 15, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Gliocladium roseum (1)
US-09-632-570-15

Query Match      82.5%; Score 33; DB 4; Length 238;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
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Db 66 DWSWS 70

RESULT 47
US-09-632-575-45
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; Sequence 45, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632,575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Gliocladium roseum (1)
US-09-632-575-45

Query Match      82.5%; Score 33; DB 4; Length 238;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DMSWA 6
      ||||:
Db      66 DMSWS 70

RESULT 48
US-09-216-295-15
; Sequence 15, Application US/09216295
; Patent No. 6268328
; GENERAL INFORMATION:
; APPLICANT: Mitchinson, Colin
; APPLICANT: Wendt, Dan J.
; TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions
; FILE REFERENCE: GC555
; CURRENT APPLICATION NUMBER: US/09/216,295
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Gliocladium roseum (1)
US-09-216-295-15

Query Match      82.5%; Score 33; DB 3; Length 239;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DMSWA 6
      ||||:
Db      66 DMSWS 70

RESULT 49
US-09-252-991A-17312
; Sequence 17312, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17312
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; LENGTH: 316
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17312

Query Match      82.5%; Score 33; DB 4; Length 316;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DMSWA 6
      ||||:
Db      272 DMSWA 276

RESULT 50
US-08-140-104A-2
; Sequence 2, Application US/08140104A
; Patent No. 5585255
; GENERAL INFORMATION:
; APPLICANT: Tsukada, Yogi
; APPLICANT: Tazuke, Yasuhiko
; APPLICANT: Okada, Shigenori
; APPLICANT: Adachi, Kenichi
; TITLE OF INVENTION: BILE ACID SULFATASE GENE, PLASMID
; TITLE OF INVENTION: CONTAINING SAID GENE AND METHOD OF PRODUCING BILE ACID
; TITLE OF INVENTION: SULFATE SULFATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/140,104A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP PCT/JP93/00244
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E.
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-140-104A-2

Query Match      82.5%; Score 33; DB 1; Length 467;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADMSW 5
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Db      401 ADMAW 405

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Job time : 20 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:18:19 ; Search time 42 Seconds
(without alignments)
44.736 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1288442 seqs, 313154207 residues

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	100.0	6	10	US-09-847-946A-41
2	40	100.0	6	10	US-09-847-946A-71
3	40	100.0	7	10	US-09-847-946A-77
4	40	100.0	8	10	US-09-847-946A-70
5	40	100.0	8	10	US-09-847-946A-78
6	40	100.0	9	10	US-09-847-946A-69
7	40	100.0	9	10	US-09-847-946A-72
8	40	100.0	9	10	US-09-847-946A-75
9	40	100.0	9	10	US-09-847-946A-76
10	40	100.0	10	10	US-09-847-946A-71
11	40	100.0	10	10	US-09-847-946A-74
12	40	100.0	11	10	US-09-847-946A-68
13	37	92.5	236	12	US-10-441-625-17
14	37	92.5	236	14	US-10-441-626-17
15	37	92.5	885	9	US-09-815-242-5090

16	37	92.5	885	12	US-10-282-122A-43572	Sequence 43572, A
17	36	90.0	6	9	US-09-847-940B-4	Sequence 4, Appli
18	36	90.0	6	9	US-09-847-940B-5	Sequence 5, Appli
19	36	90.0	6	10	US-09-847-946A-4	Sequence 4, Appli
20	36	90.0	6	10	US-09-847-946A-5	Sequence 5, Appli
21	36	90.0	6	10	US-09-847-946A-39	Sequence 39, Appl
22	36	90.0	6	10	US-09-847-946A-40	Sequence 40, Appl
23	36	90.0	6	10	US-09-847-946A-51	Sequence 51, Appl
24	36	90.0	6	10	US-09-847-946A-52	Sequence 52, Appl
25	36	90.0	6	10	US-09-847-946A-55	Sequence 55, Appl
26	36	90.0	7	10	US-09-847-946A-56	Sequence 56, Appl
27	36	90.0	8	10	US-09-847-946A-48	Sequence 48, Appl
28	36	90.0	8	10	US-09-847-946A-56	Sequence 56, Appl
29	36	90.0	8	10	US-09-847-946A-59	Sequence 59, Appl
30	36	90.0	8	10	US-09-847-946A-67	Sequence 67, Appl
31	36	90.0	9	10	US-09-847-946A-47	Sequence 47, Appl
32	36	90.0	9	10	US-09-847-946A-50	Sequence 50, Appl
33	36	90.0	9	10	US-09-847-946A-53	Sequence 53, Appl
34	36	90.0	9	10	US-09-847-946A-54	Sequence 54, Appl
35	36	90.0	9	10	US-09-847-946A-58	Sequence 58, Appl
36	36	90.0	9	10	US-09-847-946A-61	Sequence 61, Appl
37	36	90.0	9	10	US-09-847-946A-64	Sequence 64, Appl
38	36	90.0	9	10	US-09-847-946A-65	Sequence 65, Appl
39	36	90.0	10	10	US-09-847-946A-49	Sequence 49, Appl
40	36	90.0	10	10	US-09-847-946A-52	Sequence 52, Appl
41	36	90.0	10	10	US-09-847-946A-57	Sequence 57, Appl
42	36	90.0	10	10	US-09-847-946A-60	Sequence 60, Appl
43	36	90.0	10	10	US-09-847-946A-63	Sequence 63, Appl
44	36	90.0	11	10	US-09-847-946A-46	Sequence 46, Appl
45	36	90.0	147	12	US-10-424-599-199086	Sequence 199086,
46	36	90.0	173	14	US-10-156-761-15045	Sequence 15045, A
47	36	90.0	174	14	US-10-219-220-163	Sequence 163, App
48	36	90.0	225	14	US-10-219-220-162	Sequence 162, App
49	36	90.0	277	14	US-10-219-220-280	Sequence 280, App
50	36	90.0	312	14	US-10-306-762-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1:
US-09-847-946A-41
; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-41

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ADWSWA 6
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Db 1 ADWSWA 6

RESULT 2
US-09-847-946A-73
; Sequence 73, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 73
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-73

Query Match 100.0%; Score 40; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
    |||||
Db 1 ADWSWA 6

RESULT 3
US-09-847-946A-77
; Sequence 77, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-77

Query Match 100.0%; Score 40; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
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Db 1 ADWSWA 6

RESULT 4
US-09-847-946A-70
; Sequence 70, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-70

Query Match 100.0%; Score 40; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
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Db 3 ADWSWA 8

RESULT 5
US-09-847-946A-78
; Sequence 78, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-78
```

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US-09-847-946A-72
Query Match      100.0%; Score 40; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      1 ADWSWA 6

RESULT 6
US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-69

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      1 ADWSWA 6

RESULT 7
US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      1 ADWSWA 6

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-75

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8
```

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76

Query Match      100.0%; Score 40; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      2 ADWSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71

Query Match      100.0%; Score 40; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      2 ADWSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
```

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; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-74

Query Match      100.0%; Score 40; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8

RESULT 12
US-09-847-946A-68
; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-68

Query Match      100.0%; Score 40; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8

RESULT 13
US-10-441-625-17
; Sequence 17, Application US/10441625
; Publication No. US20030203467A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441,625
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
```

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; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-625-17

Query Match          92.5%; Score 37; DB 12; Length 236;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 14
US-10-441-626-17
; Sequence 17, Application US/10441626
; Publication No. US20030186418A1
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. US20030186418A1e1 Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/10/441.626
; CURRENT FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-10-441-626-17

Query Match          92.5%; Score 37; DB 14; Length 236;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      63 ADWSWS 68

RESULT 15
US-09-815-242-5090
; Sequence 5090, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815.242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43572
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-43572

Query Match          92.5%; Score 37; DB 12; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADMSWA 6
Db      563 ADWAWA 568

RESULT 16
US-10-282-122A-43572
; Sequence 43572, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43572
; LENGTH: 885
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-43572

Query Match          92.5%; Score 37; DB 12; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||||
Db 563 ADWAWA 568

RESULT 17

US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; CURRENT FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match 90.0%; Score 36; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 18

US-09-847-940B-5
; Sequence 5, Application US/09847940B
; Patent No. US2002015600A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; CURRENT FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-5

Query Match 90.0%; Score 36; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 19

US-09-847-946A-4

; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||||
Db 1 ADWSW 5

RESULT 20

US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||||
Db 2 DWSWA 6

RESULT 21

US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-39

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 22
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-40

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 23
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-51

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 24
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-62

Query Match 90.0%; Score 36; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 DWSWA 6
Db      2 DWSWA 6

RESULT 25
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-55

Query Match      90.0%; Score 36; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      1 ADWSW 5

RESULT 26
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-66

Query Match      90.0%; Score 36; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      1 ADWSW 5

RESULT 27
US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match      90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      3 ADWSW 7

RESULT 28
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-56
```

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US-09-847-946A-56
Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 29
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 4 DWSWA 8

RESULT 30
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 4 DWSWA 8

RESULT 31
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 32
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match          90.0%; Score 36; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5
```

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 33
US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 3 ADWSW 7

RESULT 34
US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
```

```
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 2 ADWSW 6

RESULT 35
US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-58

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 36
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
```

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; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-61

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      2 DWSWA 6
      |||||

RESULT 37
US-09-847-946A-64
; Sequence 64, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-64

Query Match          90.0%; Score 36; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      4 DWSWA 8
      |||||

RESULT 38
US-09-847-946A-65
; Sequence 65, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-65

Query Match          90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      2 ADWSW 6
      |||||

RESULT 40
US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
```

; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-52

Query Match 90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 3 ADWSW 7

RESULT 41
US-09-847-946A-57
; Sequence 57, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-57

Query Match 90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 3 DWSWA 7

RESULT 42
US-09-847-946A-60
; Sequence 60, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-60

Query Match 90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 3 DWSWA 7

RESULT 43
US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-63

Query Match 90.0%; Score 36; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 4 DWSWA 8

RESULT 44
US-09-847-946A-46
; Sequence 46, Application US/09847946A

Publication No. US20030054999A1
GENERAL INFORMATION:

APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findeis, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46

LENGTH: 11
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding

OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match 90.0%; Score 36; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 3 ADWSW 7

RESULT 45

US-10-424-599-199086
Sequence 199086, Application US/10424599
Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 199086
LENGTH: 147

TYPE: PRT
ORGANISM: Glycine max

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_2179C.1.pap
US-10-424-599-199086

Query Match 90.0%; Score 36; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 75 DWSWA 79

RESULT 46

US-10-156-761-15045

Sequence 15045, Application US/10156761

Publication No. US20030115018A1

GENERAL INFORMATION:

APPLICANT: OMURA, SATOSHI

APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 15045

LENGTH: 173

TYPE: PRT

ORGANISM: Streptomyces avermitilis

US-10-156-761-15045

Query Match 90.0%; Score 36; DB 14; Length 173;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 53 ADWEWA 58

RESULT 47

US-10-219-220-163

Sequence 163, Application US/10219220

Publication No. US20030082724A1

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of plant development

FILE REFERENCE: 11000.1022c1

CURRENT APPLICATION NUMBER: US/10/219,220

CURRENT FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932

PRIOR FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 290

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 163

LENGTH: 174

TYPE: PRT

ORGANISM: Eucalyptus grandis

US-10-219-220-163

Query Match 90.0%; Score 36; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 109 ADWSW 113

RESULT 48

US-10-219-220-162

Sequence 162, Application US/10219220

Publication No. US20030082724A1

GENERAL INFORMATION:

APPLICANT: Flinn, Barry

APPLICANT: Lasham, Annette

TITLE OF INVENTION: Compositions affecting programmed cell

TITLE OF INVENTION: death and their use in the modification of plant development

FILE REFERENCE: 11000.1022c1

CURRENT APPLICATION NUMBER: US/10/219,220

CURRENT FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-162

Query Match 90.0%; Score 36; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 100 ADWSW 104

RESULT 49
US-10-219-220-280
; Sequence 280, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE OF INVENTION: Death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 280
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-280

Query Match 90.0%; Score 36; DB 14; Length 277;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 95 ADWSW 99

RESULT 50
US-10-306-762-23
; Sequence 23, Application US/10306762
; Publication No. US20030187220A1
; GENERAL INFORMATION:
; APPLICANT: Park, Frances
; APPLICANT: Gajiwala, Ketan S.
; APPLICANT: Buchanan, Sean Grant
; APPLICANT: Sauder, J. Michael
; TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF A FLAVIN
; FILE OF INVENTION: MONONUCLEOTIDE BINDING PROTEIN (FMNBP)
; FILE REFERENCE: 52498-20011.00
; CURRENT APPLICATION NUMBER: US/10/306,762
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/334,132
; PRIOR FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 242
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 312
; TYPE: PRT
; ORGANISM: C. hutchinsonii (23137247)
US-10-306-762-23

Query Match 90.0%; Score 36; DB 14; Length 312;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 171 ADWSW 175

Search completed: July 23, 2004, 13:21:16
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:16:29 ; Search time 16 Seconds
(without alignments)
36.072 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 40
Sequence: 1 ADWSWA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : PIR 78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	610	2 T35222	hypothetical prote
2	37	92.5	885	2 C83441	two-component sens
3	36	90.0	374	2 B83241	conserved hypotet
4	36	90.0	889	2 E87304	TonB-dependent rec
5	34	85.0	275	2 T05822	hypothetical prote
6	34	85.0	617	2 C84922	probable protein k
7	34	85.0	1842	2 T43409	probable fatty-aci
8	34	85.0	1842	2 T38781	fatty acid synthas
9	33	82.5	132	2 S65785	mel-13a protein -
10	33	82.5	198	2 B82531	conserved hypotet
11	33	82.5	220	2 D64316	restriction modifi
12	33	82.5	232	2 S58353	CblB protein - she
13	33	82.5	239	2 D90470	hypothetical prote
14	33	82.5	257	2 D87152	conserved hypotet
15	33	82.5	276	2 B75337	hypothetical prote
16	33	82.5	304	2 F83622	probable cytochrom
17	33	82.5	310	2 JC7853	L-fucose-specific
18	33	82.5	324	2 AB3548	vegetatible incom
19	33	82.5	328	2 E72424	oligopeptide ABC t
20	33	82.5	333	2 S47246	gene CDI protein -
21	33	82.5	350	2 S71923	cysteine proteinas
22	33	82.5	368	2 H50998	probable proteinas
23	33	82.5	410	2 D75475	lycopenase cyclase -
24	33	82.5	415	2 AE1844	hypothetical prote
25	33	82.5	418	2 AB1460	sugar ABC transpor
26	33	82.5	418	2 AF1097	probable phosphata
27	33	82.5	421	2 T38242	hypothetical prote
28	33	82.5	433	2 T31511	hypothetical prote
29	33	82.5	467	2 G82697	hypothetical prote

30	33	82.5	478	2 E89790	6-phospho-beta-glu
31	33	82.5	479	2 I39953	6-phospho-beta-glu
32	33	82.5	492	2 S03098	aerolysin precursor
33	33	82.5	529	2 C86958	probable GMP synth
34	33	82.5	539	2 T15256	hypothetical prote
35	33	82.5	578	2 C64452	restriction modifi
36	33	82.5	590	2 S72813	GMP synthase (glut
37	33	82.5	616	2 C69226	type I restriction
38	33	82.5	623	2 E75221	type I restriction
39	33	82.5	765	2 S76795	hypothetical prote
40	33	82.5	836	2 D82177	conserved hypotet
41	33	82.5	1202	2 S71424	nitric-oxide synth
42	33	82.5	1203	1 A47501	nitric-oxide synth
43	33	82.5	1205	1 A38943	nitric-oxide synth
44	33	82.5	1329	2 D87226	conserved hypotet
45	33	82.5	1409	2 S74916	alkaline phosphata
46	33	82.5	1879	2 S74915	extracellular nucl
47	33	82.5	3005	2 T08841	polyprotein - dour
48	32	80.0	100	2 H81042	hypothetical prote
49	32	80.0	107	1 SSUL	stellacyanin - Jap
50	32	80.0	113	2 A75355	hypothetical prote

ALIGNMENTS

RESULT 1
T35222
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C/Accession: T35222
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A/Reference number: Z21572
A/Accession: T35222
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-610 <SEE>
A/Cross-references: EMBL:AL031515; PIDN:CAA20627.1; GSPDB:GN00070; SCOEDB:SC5C7.15
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOEDB:SC5C7.15

Query Match 92.5%; Score 37; DB 2; Length 610;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 83 ADWAWA 88

RESULT 2
C83441
two-component sensor KdpD PA1636 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: C83441
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83441
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-885 <STO>
A/Cross-references: GB:AE004591; GB:AE004091; NID:g9947599; PIDN:AAG05025.1; GSPDB:GN0011
A/Experimental source: strain PA01
C/Genetics:
A/Gene: kdpD; PA1636

Query Match 92.5%; Score 37; DB 2; Length 885;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 563 ADMAWA 568
|||||

RESULT 3
B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83241
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:2043737; PMID:10984043
A;Accession: B83241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN00148
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3230

Query Match 90.0%; Score 36; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 81 DWSWA 85
|||||

RESULT 4
E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87304
R;Nierman, W.C.; Felchlyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <STO>
A;Cross-references: GB:AE005673; NID:g13421615; PIDN:AAK22433.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0446

Query Match 90.0%; Score 36; DB 2; Length 889;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 618 ADWSW 622
|||||

RESULT 5
T05822
hypothetical protein TSK18.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T05822
R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Bar
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15453
A;Accession: T05822
A;Molecule type: DNA
A;Residues: 1-275 <BEV>
A;Cross-references: EMBL:AL022580
A;Experimental source: cultivar Columbia; BAC clone T5K18
C;Genetics:
A;Map position: 4
A;Intons: 103/3; 141/3; 169/1; 206/3
A;Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 57 SDWSWS 62
|||||

RESULT 6
C84922
probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84922
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Kneusel, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-617 <STO>
A;Cross-references: GB:AE002093; NID:g4249408; PIDN:AAD13705.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g48010
A;Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 500 ADMAWS 505
|||||

RESULT 7
T43409
Probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: fatty acid synthetase alpha subunit
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T43409
R;Saichon, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.; Yanagida, M.; Cell Biol. 134, 949-961, 1996
A;Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase and
A;Reference number: Z22493; MUID:96354912; PMID:8769419
A;Accession: T43409
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1842 <SAI>
A;Cross-references: EMBL:D83412; NID:g1199959; PIDN:BAAL1913.1; PID:g1199960
C;Genetics:
A;Note: lad1+
C;Superfamily: yeast fatty-acid synthase

C;Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
:|:|:
Db 400 SDMNWA 405

RESULT 8
T38781
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T38781
R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A;Reference number: 221751
A;Accession: T38781
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1842 <SKE>
A;Cross-references: EMBL:Z98762; PIDN:CAB11481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c
A;Experimental source: strain 972h-; cosmid c4A8
C;Genetics:
A;Gene: SPDB:SPAC4A8.11c
A;Map position: 1
C;Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
:|:|:
Db 400 SDMNWA 405

RESULT 9
S65785
mel-13a protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C;Accession: S65785
R;Tsetu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A;Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A;Reference number: S65785; MUID:96180310; PMID:8597592
A;Accession: S65785
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <TET>
A;Cross-references: EMBL:U35309
C;Genetics:
A;Gene: mel-13
C;Superfamily: mouse mel-13a protein
C;Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;
Best Local Similarity 80.0%; Pred. No. 96;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
:|:|:
Db 57 SDWSW 61

RESULT 10
B82531
conserved hypothetical protein XP2666 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Nov-2000
C;Accession: B82531
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below

A;Accession: B82531
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-198 <SIM>
A;Cross-references: GB:AE004072; GB:AE003849; NID:g9107884; PIDN:AAF85463.1; GSPDB:GN0012;
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; Laigret,
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret,
J.D.; Junqueira, M.L.; Kemp, E.L.; Madeira, H.M.P.; Marino, C.L.; Marques, M.V.; Martins, E.
chado, M.A.; Madeira, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki,
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira,
M.; Tuhato, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XP2666
C;Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
:|:|:
Db 135 DWNWA 139

RESULT 11
D64316
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2002
C;Accession: D64316
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, A.;
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: D64316
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A;Residues: 1-220 <BUL>
A;Cross-references: GB:U67470; GB:L77117; NID:g2826247; PIDN:AAB98113.1; PID:g1592267; T
C;Genetics:
A;Map position: REV127472-126810
A;Start codon: TTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
:|:|:
Db 33 ADWAW 37

RESULT 12

S58353
CD1b protein - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: S58353
R;Ferguson, E.D.; Dutia, B.M.; Hein, W.; Hopkins, J.
submitted to the EMBL Data Library, July 1995
A;Description: The ovine CD1 gene family contains at least four CD1B homologues.
A;Reference number: S58353
A;Accession: S58353
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-232 <FER>
A;Cross-references: EMBL:X90567; NID:g945010; PIDN:CAA62187.1; PID:g945011
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 156 ADWTW 160

RESULT 13
D90470
hypothetical protein cyeh [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: D90470
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, H-
arrett, R.A.; Ragan, M.A.; Sensesen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: D90470
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-239 <KUR>
A;Cross-references: GB:AE006641; NID:gl3816282; PIDN:AAK43019.1; GSPDB:GN00155
C;Genetics: cyh
A;Gene: cyh
C;Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 172 ADWTW 176

RESULT 14
D87152
conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: D87152
R;Cole, S.R.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87152
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO>

Query Match 82.5%; Score 33; DB 2; Length 304;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||:|

A;Cross-references: GB:AL450380; NID:gl3093601; PIDN:CAC30900.1; GSPDB:GN00147
C;Genetics:
A;Gene: ML1945
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1100

Query Match 82.5%; Score 33; DB 2; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
|||:|
Db 11 ATWSWA 16

RESULT 15
B75337
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C;Accession: B75337
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F-
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma-
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <WHI>
A;Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF11479.1; PID:g6459715
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1923
A;Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
|||:|
Db 84 ADWAW 88

RESULT 16
F83632
probable cytochrome c oxidase assembly factor PA0113 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83632
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Bri-
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen.
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83632
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <STO>
A;Cross-references: GB:AE004449; GB:AE004091; NID:g9945928; PIDN:AAG03503.1; GSPDB:GN001:
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA0113
C;Superfamily: heme O synthase

Query Match 82.5%; Score 33; DB 2; Length 304;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
|||:|

Db 260 DWAWA 264

RESULT 17

JC7853

L-fucose-specific lectin - Aspergillus oryzae

C/Species: Aspergillus oryzae

C/Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 31-Mar-2003

C/Accession: JC7853; PC7191

R/Ishida, H.; Moritani, T.; Hata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, S.

BioSci. Biotechnol. Biochem. 66, 1002-1008, 2002

A/Title: Molecular cloning and overexpression of fLeA gene encoding a fucose-specific lectin

A/Reference number: JC7853; MUID:22087106; PMID:12092808

A/Accession: JC7853

A/Molecule type: DNA

A/Residues: 1-310 <ISH>

A/Cross-references: DDBJ:AB072379

A/Experimental source: strain OSI1018

A/Accession: PC7191

A/Molecule type: protein

A/Residues: 132-147;148-177 <IS2>

C/Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity against

C/Genetics:

A/Gene: fLeA

A/Introns: 12/1; 71/3; 143/1; 177/2

Query Match 82.5%; Score 33; DB 2; Length 310;

Best Local Similarity 66.7%; Pred. No. 2.3e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 290 SEWSWA 295

RESULT 18

AB3548

vegetable incompatibility protein het-e-1 [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C/Accession: AB3548

R/DalVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, .; Mazur, M.; Gottsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letesha Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AB3548

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-324 <KUR>

A/Cross-references: GB:AE008918; PIDN:AAL53549.1; PID:gl7984458; GSPDB:GN00191

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BMEI10307

A/Map position: II

Query Match 82.5%; Score 33; DB 2; Length 324;

Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6

Db 209 DWSWS 213

RESULT 19

E72424

oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MS88)

C/Species: Thermotoga maritima

C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C/Accession: E72424

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.J.

C.M.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequencing

A/Reference number: A72200; MUID:99287316; PMID:10360571

A/Accession: E72424

A/Molecule type: DNA

A/Status: preliminary

A/Residues: 1-328 <ARN>

A/Cross-references: GB:AE001692; GB:AE000512; NID:g4980535; PIDN:AAD35154.1; PID:g4980546

A/Experimental source: strain MS88

C/Genetics:

A/Gene: TW0060

C/Superfamily: oligopeptide permease protein oppB

Query Match 82.5%; Score 33; DB 2; Length 328;

Best Local Similarity 83.3%; Pred. No. 2.4e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6

Db 181 APWSWA 186

RESULT 20

S47246

gene CD1 protein - sheep

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C/Accession: S47246

R/Ferguson, E.E.

A/Submitted to the EMBL Data Library, August 1994

A/Description: Isolation and analysis of cDNA seEncoding the ovine homologues of CD1.

A/Reference number: S47246

A/Accession: S47246

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-333 <FER>

A/Cross-references: EMBL:Z36892

C/Superfamily: class I histocompatibility antigen; immunoglobulin homology

F;216-281/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 333;

Best Local Similarity 80.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5

Db 257 ADWTW 261

RESULT 21

S71923

cysteine proteinase (EC 3.4.22.-) - garden pea

C/Species: Pisum sativum (garden pea)

C/Date: 04-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 20-Jun-2000

C/Accession: S71923

R/Jones, C.G.; Tucker, G.A.; Lycett, G.W.

Biochim. Biophys. Acta 1296, 13-15, 1996

A/Title: Pattern of expression and characteristics of a cysteine proteinase cDNA from pea

A/Reference number: S71923; MUID:96350414; PMID:8765223

A/Accession: S71923

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-350 <JON>

A/Cross-references: EMBL:Z68291; NID:gl134881; PIDN:CAA92583.1; PID:gl134882

C/Superfamily: papain

C/Keywords: cysteine proteinase; hydrolase

F;157,297,317/Active site: Cys, His, Asn #status predicted

Query Match 82.5%; Score 33; DB 2; Length 350;

Best Local Similarity 80.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	ADMSW 5		
Db	100	ADMTW 104		
RESULT 22				
H90998				
Probable proteinase/scaffold protein [imported] - Escherichia coli (strain O157:H7, subsp. probabie, Escherichia coli				
C;Species: Escherichia coli				
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001				
C;Accession: H90998				
R;Hayaishi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G. gasawara, N.; Yaginaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.				
DNA Res. 8, 11-22, 2001				
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome				
A;Reference number: A99629; MUID:21156231; PMID:11258796				
A;Accession: H90998				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-368 <HAY>				
A;Cross-references: GB:BA000007; PIDN:BA836383.1; PID:gl3362429; GSPDB:GN00154				
A;Experimental source: strain O157:H7, substrain RMD 0509952				
C;Genetics:				
A;Gene: ECs2960				
Query Match 82.5%; Score 33; DB 2; Length 368;				
Best Local Similarity 66.7%; Pred. No. 2.7e+02;				
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;				
QY	1	ADMSWA 6		
Db	32	ADMGWS 37		
RESULT 23				
D75475				
Lycopene cyclase - Deinococcus radiodurans (strain R1)				
C;Species: Deinococcus radiodurans				
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000				
C;Accession: D75475				
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.				
Science 286, 1571-1577, 1999				
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.				
A;Reference number: A75250; MUID:20036896; PMID:10567266				
A;Accession: D75475				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-410 <WHI>				
A;Cross-references: GB:AB001934; GB:AB000513; NID:g6458504; PIDN:AAF10377.1; PID:g645851				
A;Experimental source: strain R1				
C;Genetics:				
A;Gene: DR0801				
A;Map position: 1				
Query Match 82.5%; Score 33; DB 2; Length 410;				
Best Local Similarity 80.0%; Pred. No. 3e+02;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ADMSW 5		
Db	102	ADMTW 106		
RESULT 24				
A81844				
Hypothetical protein alr0301 [imported] - Nostoc sp. (strain PCC 7120)				
C;Species: Nostoc sp. PCC 7120				
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120				
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002				
C;Accession: A81844				
R;Kaneke, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi				

Nakazaki, N.; Shimpoo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yaeuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001				
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena				
A;Reference number: AB1807; MUID:21595285; PMID:11759840				
A;Accession: AE1844				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-415 <KUR>				
A;Cross-references: GB:BA000019; PIDN:BA877825.1; PID:gl7135279; GSPDB:GN00179				
A;Experimental source: strain PCC 7120				
C;Genetics:				
A;Gene: alr0301				
C;Superfamily: Synchocystis hypothetical protein sl11399				
Query Match 82.5%; Score 33; DB 2; Length 415;				
Best Local Similarity 80.0%; Pred. No. 3e+02;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	2	DMSWA 6		
Db	22	DMSWS 26		
RESULT 25				
AE1460				
sugar ABC transporter, sugar-binding protein homolog lin0220 [imported] - Listeria innocua				
C;Species: Listeria innocua				
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001				
C;Accession: AE1460				
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.				
Science 294, 849-852, 2001				
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.				
A;Reference number: AB1077; MUID:21537279; PMID:11679669				
A;Accession: AE1460				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-418 <GLA>				
A;Cross-references: GB:AL592022; PIDN:CAC95453.1; PID:gl6412639; GSPDB:GN00178				
A;Experimental source: strain Clp11262				
C;Genetics:				
A;Gene: lin0220				
Query Match 82.5%; Score 33; DB 2; Length 418;				
Best Local Similarity 80.0%; Pred. No. 3.1e+02;				
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				
QY	1	ADMSW 5		
Db	167	ADMTW 171		
RESULT 26				
AF1097				
sugar ABC transporter, sugar-binding protein homolog lmo0181 [imported] - Listeria monocytogenes				
C;Species: Listeria monocytogenes				
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001				
C;Accession: AF1097				
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.				
Science 294, 849-852, 2001				
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.				
A;Reference number: AB1077; MUID:21537279; PMID:11679669				
A;Accession: AF1097				
A;Status: preliminary				
A;Molecule type: DNA				
A;Residues: 1-418 <GLA>				

A;Cross-references: GB:NC_003210; PIDN:CAC98396.1; PID:g16409538; GSPDB:GN001177
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo0181

Query Match 82.5%; Score 33; DB 2; Length 418;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 167 ADWTW 171

RESULT 27
 T38242
 probable phosphatase - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T38242
 R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: Z21781
 A;Accession: T38242
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-421 <BRO>
 A;Cross-references: EMBL:Z98559; PIDN:CAB11157.1; GSPDB:GN000666; SPDB:SPAC23C11.04c
 A;Experimental source: strain 972h; cosmid c23C11
 C;Genetics:
 A;Gene: SPDB:SPAC23C11.04c
 A;Map position: 1
 A;Introns: 181/1; 373/3

Query Match 82.5%; Score 33; DB 2; Length 421;
 Best Local Similarity 80.0%; Pred. No. 3.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 93 ADWTW 97

RESULT 28
 T31511
 hypothetical protein Y116A8C.9 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
 C;Accession: T31511
 R;McMurray, A.
 submitted to the EMBL Data Library, October 1999
 A;Reference number: Z21041
 A;Accession: T31511
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-433 <WIL>
 A;Cross-references: EMBL:ALJ17204; PIDN:CAB55145.1; CESP:Y116A8C.9
 A;Experimental source: clone Y116A8C
 C;Genetics:
 A;Gene: CESP:Y116A8C.9
 A;Introns: 16/2; 42/2; 75/2; 107/3; 173/3; 230/3; 262/3; 318/3; 373/1; 398/1
 C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.9

Query Match 82.5%; Score 33; DB 2; Length 433;
 Best Local Similarity 80.0%; Pred. No. 3.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DWSWA 6
 Db 175 DWTWA 179

RESULT 29

G82697
 hypothetical protein XF1318 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C;Accession: G82697
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen-
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: G82697
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-467 <SIM>
 A;Cross-references: GB:AE003964; GB:AE003849; NID:g9106300; PIDN:AAF84127.1; GSPDB:GN001177
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A.
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohne
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.S.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.P.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF1318

Query Match 82.5%; Score 33; DB 2; Length 467;
 Best Local Similarity 80.0%; Pred. No. 3.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 9 ADWAW 13

RESULT 30
 E89790
 6-phospho-beta-glucosidase [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: E89790
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Z
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: E89790
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-478 <KUR>
 A;Cross-references: GB:BA000018; PID:g13700182; PIDN:BA041480.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: bglA
 C;Superfamily: Agrobacterium beta-glucosidase

Query Match 82.5%; Score 33; DB 2; Length 478;
 Best Local Similarity 66.7%; Pred. No. 3.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ADWSWA 6
 Db 347 SDWGWA 352

RESULT 31
I39953
6-phospho-beta-glucosidase (EC 3.2.1.86) bgIA - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C/Accession: I39953; F69593
R/Zhang, J.; Aronson, A.I.
Gene 140, 85-90, 1994
A/Title: A Bacillus subtilis bgIA gene encoding phospho-beta-glucosidase is inducible an
A/Reference number: I39953; MUID:94171085; PMID:8125345
A/Accession: I39953
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-479 <RES>
A/Cross-references: GB:I19710; NID:g506380; PIDN:AAA2660.1; PID:g506381
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea
C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Patro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: F69593
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-479 <KUN>
A/Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16048.1; PID:g2636558
A/Experimental source: strain 168
C/Genetics:
A/Gene: bgIA
C/Superfamily: Agrobacterium beta-glucosidase
C/Keywords: glycosidase; hydrolase
Query Match 82.5%; Score 33; DB 2; Length 479;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 347 SDWGWA 352
RESULT 32
S03098
aerolysin precursor - Aeromonas sobria
C/Species: Aeromonas sobria
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 10-Dec-1999
C/Accession: S03098
R/Hussein, V.; Huhle, B.; Jarchau, T.; Lurz, R.; Goebel, W.; Chakraborty, T.
Mol. Microbiol. 2, 507-517, 1988
A/Title: Nucleotide sequence and transcriptional analysis of the aerCaerA region of Aero
A/Reference number: S03097; MUID:89013892; PMID:2459581
A/Accession: S03098
A/Molecule type: DNA
A/Residues: 1-492 <HUS>
A/Cross-references: EMBL:Y00559; NID:g39016; PIDN:CAA68642.1; PID:g39018
A/Note: part of this sequence, including the amino end of the mature protein, was confi
C/Genetics:
A/Gene: aerA
C/Superfamily: aerolysin
F,1-23/Domain: signal sequence #status predicted <SIG>
F,24-492/Product: aerolysin #status predicted <MAT>
Query Match 82.5%; Score 33; DB 2; Length 492;

Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 395 DWNWA 399

RESULT 33

C86958
probable GMP synthase [imported] - Mycobacterium leprae

C/Species: Mycobacterium leprae

C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001

C/Accession: C86958

R/Coile, S.T.; Eiglmier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor

R.; Davies, R.M.; Davlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A/Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A/Title: Massive gene decay in the leprosy bacillus.

A/Reference number: A86909; MUID:21128732; PMID:11234002

A/Accession: C86958

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-529 <STO>

A/Cross-references: GB:AL450380; NID:gl3092668; PIDN:CAC29903.1; GSPDB:GN00147

C/Genetics:

A/Gene: guaA

C/Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology

Query Match 82.5%; Score 33; DB 2; Length 529;

Best Local Similarity 80.0%; Pred. No. 3.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 487 ADWTW 491

RESULT 34

T15256

hypothetical protein K07B1.7 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T15256

R/Pauley, A.; Gattung, S.

submitted to the EMBL Data Library, May 1997

A/Description: The sequence of C. elegans cosmid K07B1.

A/Reference number: Z18317

A/Accession: T15256

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-539 <PAU>

A/Cross-references: EMBL:AF003384; NID:g2088817; PID:g2088823; PIDN:AA54241.1; GSPDB:GN

A/Experimental source: strain Bristol N2; clone K07B1

C/Genetics:

A/Gene: CESP:K07B1.7

A/Map position: 5

A/Introns: 34/1; 79/3; 313/1; 355/2; 406/2; 466/2; 500/2

Query Match 82.5%; Score 33; DB 2; Length 539;

Best Local Similarity 80.0%; Pred. No. 3.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DMSWA 6
Db 317 DWAWA 321

RESULT 35

C64452

restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii

C/Species: Methanococcus jannaschii

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: C64452
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Ison, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8698087
A;Accession: C64452
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-578 <BUL>
A;Cross-references: GB:U67563; GB:L77117; NID:G2826379; PIDN:AAB99225.1; PID:GLS92326; T
C;Genetics:
A;Map position: REV1163994-1162258
A;Start codon: TTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 578;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 391 ADMAW 395
|||:|

RESULT 36
S72813
GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) - Mycobacterium leprae
N;Alternate names: GMP synthetase guaA; protein Bl620_C2_205
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C;Accession: S72813
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid Bl620.
A;Reference number: S72594
A;Accession: S72813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-590 <SMI>
A;Cross-references: EMBL:U00015; NID:G466931; PIDN:AAC43222.1; PID:G466934
C;Genetics:
A;Gene: guaA
C;Superfamily: GMP synthase (glutamine-hydrolyzing); trpG homology
C;Keywords: ligase; purine nucleotide biosynthesis
F;78-257/Domain: trpG homology <TRG>
F;298-465/Domain: GMP binding #status predicted <GMP>
F;154/Active site: Cys #status predicted

Query Match 82.5%; Score 33; DB 2; Length 590;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 548 ADWTM 552
|||:|

RESULT 37
C69226
type I restriction modification enzyme, subunit M - Methanobacterium thermoautotrophicum
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: C69226
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N. ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: C69226
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-616 <MTH>
A;Cross-references: GB:AE000868; GB:AE000666; NID:G2622025; PIDN:AAB85440.1; PID:G2622040
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH942
A;Start codon: GTG
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 616;
Best Local Similarity 80.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 425 ADMAW 429
|||:|

RESULT 38
E75221
type I restriction modification enzyme, chain m. PAB2149 - Pyrococcus abyssi (strain Orai
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: E75221
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
A;Accession: E75221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-623 <KAW>
A;Cross-references: GB:AJ248283; GB:AL096836; NID:G5457433; PIDN:CAB49220.1; PID:G5457725
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB2149
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 82.5%; Score 33; DB 2; Length 623;
Best Local Similarity 80.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 434 ADMAW 438
|||:|

RESULT 39
S76795
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C;Species: Synecocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S76795
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76795
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-765 <KAN>
A;Cross-references: EMBL:D90916; GB:AB001339; NID:G1653715; PIDN:BAA18707.1; PID:dl019440
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 82.5%; Score 33; DB 2; Length 765;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

A:Gene: GDB:NOS3
A:Cross-references: GDB:209976; OMIM:163729
A:Map position: 7q36-7q36
A:Introns: 53/2; 90/3; 140/2; 194/3; 225/2; 272/3; 319/2; 377/3; 411/3; 476/3; 501/2; 54
C:Function:
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C:Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN
F:491-509/Region: calmodulin binding #status predicted
F:520-1159/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:522-703/Domain: flavodoxin homology <FLX>
F:648-680/Region: FMN binding #status predicted
F:791-804/Region: FAD-pyrophosphate binding #status predicted
F:935-946/Region: FAD-isalloxazine binding #status predicted
F:1010-1028/Region: NADP-ribose binding #status predicted
F:1108-1124/Region: NADP-adenine binding #status predicted
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:184/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 1203;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 443 ADMAW 447

RESULT 43
A:38943
nitric-oxide synthase (EC 1.14.13.39), endothelial - bovine
N:Alternate names: ECNOS; nitric-oxide synthase type III
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text change 03-Mar-2000
C:Accession: A38943; J45945; A42841; I45946; A38944
R:Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
submitted to GenBank, July 1992
A:Reference number: A38943
A:Accession: A38943
A:Molecule type: mRNA
A:Residues: 1-1205 <LAM1>
A:Cross-references: GB:M9952; NID:g162976; PIDN:AAA30494.1; PID:g162977
A:Experimental source: aortic endothelial cells
R:Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 6348-6352, 1992
A:Title: Endothelial nitric oxide synthase: molecular cloning and characterization of a
A:Reference number: A46033; MUID:92335295; PMID:1378626
A:Accession: A46033
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-860, 'I', 862-1205 <LAM2>
A:Cross-references: GB:M9952; NID:g162976
A:Experimental source: endothelial
A:Note: sequence extracted from NCBI backbone (NCBIP:108720)
R:Nishida, K.; Harrison, D.G.; Navas, J.P.; Fisher, A.A.; Dockery, S.P.; Nerem, R.M.; Al
J. Clin. Invest. 90, 2092-2096, 1992
A:Title: Molecular Cloning and Characterization of the constitutive bovine aortic Endoth
A:Reference number: 145945; MUID:93055452; PMID:1385480
A:Accession: 145945
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1205 <NIS>
A:Cross-references: GB:M99057; NID:g163421; PIDN:AAA30667.1; PID:g163422
R:Seega, W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
J. Biol. Chem. 267, 15274-15276, 1992
A:Title: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi
A:Reference number: A42841; MUID:92348367; PMID:1379225
A:Accession: A42841
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-51, 'N', 53-99, 'R', 101-147, 'M', 149-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-3
'K', 517-692, 'G', 694-740, 'A', 742-753, 'N', 755-799, 'N', 801-803, 'SA', 806-856, 'V', 858-906, 'LV

A:Experimental source: aortic endothelial cells
A:Note: sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typogr
A:Accession: I45946
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-99, 'R', 101-164, 'I', 166-317, 'GA', 320, 'HTGVVRGP', 329-454, 'Y', 456-458, 'P', 460-
A:Cross-references: GB:M95674; NID:g163426; PIDN:AAA30669.1; PID:g163427
A:Experimental source: aortic endothelial cells
A:Note: submitted to GenBank, August 1992
A:Note: GenBank entry BOVNO5, release 103.0, has a typographical error in the reference
C:Function:
A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C:Keywords: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN;
F:493-512/Region: calmodulin binding #status predicted
F:522-1161/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F:524-705/Domain: flavodoxin homology <FLX>
F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F:3/Modified site: aspartic acid (Asn) #status predicted
F:186/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 82.5%; Score 33; DB 1; Length 1205;
Best Local Similarity 80.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 445 ADMAW 449

RESULT 44
D87226
conserved hypothetical protein ML2535 [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: D87226
R:Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holtroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D87226
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1329 <STO>
A:Cross-references: GB:AL450380; NID:g13093796; PIDN:CAC32066.1; GSPDB:GN00147
C:Genetics:
A:Gene: ML2535

Query Match 82.5%; Score 33; DB 2; Length 1329;
Best Local Similarity 80.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 260 SDMSW 264

RESULT 45
S74916
alkaline phosphatase - Synecocystis sp. (strain PCC 6803)
N:Alternate names: protein sl10654
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
S.

A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74916
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1409 <KAN>
A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAAL6956.1; PID:d101768
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 82.5%; Score 33; DB 2; Length 1409;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADNSW 5
Db 1370 ADMNW 1374

RESULT 46

S74915
extracellular nuclease - *Synechocystis* sp. (strain PCC 6803)
N;Alternate names: protein sl10656
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S74915
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
S.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74915
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1879 <KAN>
A;Cross-references: EMBL:D90902; GB:AB001339; NID:g1652027; PIDN:BAAL6955.1; PID:d101768
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: nuch
A;Start codon: GTG

Query Match 82.5%; Score 33; DB 2; Length 1879;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADNSW 5
Db 1847 ADMNW 1851

RESULT 47

T08841
polyprotein - douroucouli hepatitis GB virus A
C;Species: douroucouli hepatitis GB virus A
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C;Accession: T08841
R;Erker, J.C.; Desai, S.M.; Leary, T.P.; Chalmers, M.L.; Montes, C.C.; Mushahwar, I.K.
J. Gen. Virol. 79, 41-45, 1998
A;Title: Genomic analysis of two GB virus A variants isolated from captive monkeys.
A;Reference number: 216486; MUID:98120818; PMID:9460920
A;Accession: T08841
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3005 <ERK>
A;Cross-references: EMBL:AF023425; NID:g2828599; PIDN:AAC40502.1; PID:g2828600
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein

Query Match 82.5%; Score 33; DB 2; Length 3005;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADNSW 5

Db 759 SDWSW 763

RESULT 48

H81042
hypothetical protein NMB1782 [imported] - *Neisseria meningitidis* (strain MC58 serogroup F)
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: H81042; G81988
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <TET>
A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42122.1; PID:g722703;
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morelli
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83970.1; PID:g7379120
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1782; NMA0683; NMA0684
C;Superfamily: *Neisseria meningitidis* hypothetical protein NMB1782

Query Match 80.0%; Score 32; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 77 DWSW 80

RESULT 49

SSUL
stellacyanin - Japanese lacquer-tree
C;Species: *Rhus vernicifera* (Japanese lacquer-tree)
C;Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 04-Nov-2002
C;Accession: A00311
R;Bergman, C.; Gandvik, E.K.; Nyman, P.O.; Strid, L.
Biochem. Biophys. Res. Commun. 77, 1052-1059, 1977
A;Title: The amino acid sequence of stellacyanin from the lacquer tree.
A;Reference number: A90206; MUID:77266668; PMID:901509
A;Accession: A00311
A;Molecule type: protein
A;Residues: 1-107 <BER>
R;Bergman, C.; Gandvik, E.K.; Nyman, P.O.; Strid, L.
Biochem. Biophys. Res. Commun. 79, 1013, 1977
A;Reference number: A90207
A;Contents: annotation; erratum
R;Engeseth, H.R.; Hermanson, M.A.; McMillin, D.R.
FEBS Lett. 171, 257-261, 1984
A;Title: A new assignment of the disulfide linkage in stellacyanin.
A;Reference number: A91324; MUID:84208877; PMID:6723985
A;Contents: annotation; disulfide bond
C;Comment: This is a blue, type 1 copper glycoprotein.
C;Superfamily: stellacyanin
C;Keywords: copper; electron transfer; glycoprotein
F;28,60,102/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;46,87,92,97/Binding site: copper (His, Cys, His, Gln) #status predicted
F;53-93/Disulfide bonds: #status experimental

Query Match 80.0%; Score 32; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||
Db 22 DWKWA 26

RESULT 50

A75355
Hypothetical protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C/Accession: A75355
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: A75355
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-113 <WHI>
A/Cross-references: GB:AE002019; GB:AE00513; NID:g6459547; PIDN:AAF11336.1; PID:g645955
A/Experimental source: strain R1
C/Genetics:
A/Gene: DRI779
A/Map position: 1

Query Match 80.0%; Score 32; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||
Db 28 DWKWA 32

Search completed: July 23, 2004, 13:19:54
Job time : 17 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:14:03 ; Search time 14 Seconds
(without alignments)
22.316 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	470	1 NRAM_IADBU	Q07570 influenza a
2	36	90.0	470	1 NRAM_IADCH	Q07571 influenza a
3	36	90.0	470	1 NRAM_IADH2	Q07572 influenza a
4	36	90.0	470	1 NRAM_IADM2	Q07573 influenza a
5	36	90.0	470	1 NRAM_IADU3	Q07599 influenza a
6	36	90.0	470	1 NRAM_IAGFN	Q07574 influenza a
7	36	90.0	470	1 NRAM_IAGHD	Q07577 influenza a
8	36	90.0	470	1 NRAM_IAHJI	Q07578 influenza a
9	36	90.0	470	1 NRAM_IAMAE	Q07583 influenza a
10	36	90.0	470	1 NRAM_IATKL	Q07585 influenza a
11	36	90.0	598	1 MRJ5_APIME	Q07432 epis mellif
12	34	85.0	376	1 PGLR_PENGR	O93883 penicillium
13	34	85.0	1842	1 PAS2_SCHPO	Q10289 s fatty aci
14	33	82.5	99	1 NOS3_SHEEP	P79209 ovis aries
15	33	82.5	220	1 Y132_METJA	Q57596 methanococ
16	33	82.5	232	1 C1B3_SHEEP	P80943 ovis aries
17	33	82.5	333	1 C1B2_SHEEP	Q29422 ovis aries
18	33	82.5	410	1 Y801_DEIRA	Q9rw68 deinococcus
19	33	82.5	421	1 PNK1_SCHPO	O13911 schizosacch
20	33	82.5	470	1 NRAM_IQAOT	Q07584 influenza a
21	33	82.5	479	1 BGLA_BACSU	P42973 bacillus su
22	33	82.5	492	1 AERA_AERTR	P09166 aeromonas t
23	33	82.5	529	1 GUAA_MYCLE	P46810 mycobacteri
24	33	82.5	578	1 YC20_METJA	Q58617 methanococ
25	33	82.5	579	1 YC12_KLRPN	Q48458 klebsiella
26	33	82.5	817	1 PHK_STRCO	Q8ck51 streptomyce
27	33	82.5	914	1 GUX2_CLOSOR	P50900 clostridium
28	33	82.5	1201	1 NOS3_MOUSE	P70313 mus musculu
29	33	82.5	1202	1 NOS3_HUMAN	P29474 homo sapien
30	33	82.5	1204	1 NOS3_BOVIN	P29473 bos taurus
31	33	82.5	1204	1 NOS3_PIG	Q28969 sus scrofa
32	32	80.0	100	1 NOS3_CAVPO	P97270 cavia porce
33	32	80.0	107	1 STEL_RHUVF	P00302 rhus vernic

34	32	80.0	125	1 VG61_BPMD2	O64253 mycobacteri
35	32	80.0	272	1 CY1_RHURU	P23135 rhodospiril
36	32	80.0	282	1 3MG2_ECOLI	P04395 escherichia
37	32	80.0	295	1 X769_HUMAN	P99871 homo sapien
38	32	80.0	339	1 YJGB_ECOLI	P27250 escherichia
39	32	80.0	360	1 WNT2_CABEL	P34889 caenorhabdi
40	32	80.0	362	1 DCUP_YEAST	P32347 saccharomyc
41	32	80.0	375	1 HIS2_XANCP	P58882 xanthomonas
42	32	80.0	411	1 POLC_BUCAI	P57285 buchnera ap
43	32	80.0	418	1 HLT_VIBPA	P99289 vibrio para
44	32	80.0	453	1 NRAM_IAPUE	P03470 influenza a
45	32	80.0	454	1 NRAM_IAPUE	P03468 influenza a
46	32	80.0	470	1 NOS2_ONCMY	Q92091 oncorhynchu
47	32	80.0	483	1 ENGA_BRUME	Q8yfh2 bruceella me
48	32	80.0	483	1 ENGA_BRUSU	Q8g288 bruceella su
49	32	80.0	536	1 YC42_SYNY3	P42349 synechocyst
50	32	80.0	601	1 DNJM_MYCGE	P47442 mycoplasma

ALIGNMENTS

RESULT 1

NRAM_IADBU

ID_NRAM_IADBU STANDARD; PRT; 470 AA.

AC Q07570;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuraminidase [EC 3.2.1.18].

GN NA.

OS Influenza A virus (strain A/Duck/Burjatia/652/88).

OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

OC Influenza A viruses; Influenzavirus A.

OX NCBI_TaxID=38956;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93212520; PubMed=8460490;

RA Saito T., Kawaoka Y., Webster R.G.;

RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A

RL Virology 193:868-876(1993).

CC -I- FUNCTION: Removes the terminal sialic acid from carbohydrate side

CC chains of the host cell surface proteins and from the viral

CC envelope. Such a reaction prevents self-aggregation and facilitate

CC the mobility of the virus to and from the site of infection.

CC -I- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,

CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in

CC oligosaccharides, glycoproteins, glycolipids, colominic acid and

CC synthetic substrates.

CC -I- SUBUNIT: Homotetramer.

CC -I- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped

CC spike on the surface of the virion.

CC -I- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; L06572; AAA43365.1; -.

CC HSP; P06820; 2BAT.

CC InterPro; IPR001860; Glyco_hydro_34.

CC Pfam; PF00064; neur; 1.

CC ProDom; PD000431; Glyco_hydro_34; 1.

CC Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

CC TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

CC DOMAIN 39 88 HYPERVARIABLE STALK REGION.

CC DOMAIN 89 470 HEAD OF NEURAMINIDASE.

CC ACT_SITE 273 273 BY SIMILARITY.

FT	ACT_SITE	275	275	BY SIMILARITY.
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	54	54	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	144	144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	470 AA;	51989 MW; DIA6F07460F6F8AD CRC64;	
Query Match				
Best Local Similarity 90.0%; Score 36; DB 1; Length 470;				
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ADWSW 5			
Dd	453 ADMSW 457			
RESULT 2				
ID	NRAM_IADCH	STANDARD;	PRT;	470 AA.
AC	Q07571;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuraminidase (EC 3.2.1.18).			
GN	NA.			
OS	Influenza A virus (strain A/Duck/Chabarovsk/1610/72).			
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC	Influenza A viruses; Influenzavirus A.			
OX	NCBI_TaxID=38957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93212520; PubMed=8460490;			
RA	Saito T., Kawaoka Y., Webster R.G.;			
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";			
RL	Virology 193:868-876(1993).			
CC	- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.			
CC	- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.			
CC	- SUBUNIT: Homotetramer.			
CC	- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.			
CC	- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.			
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EMBL; L06573; AAA43367.1; -.				
HSSP; P06820; 2BAT.				
InterPro; IPR001860; Glyco_hydro_34.				
Pfam; PF00064; neur; 1.				
ProDom; PD000431; Glyco_hydro_34; 1.				
TRANSMEM 7 38	ANCHOR (BY SIMILARITY).			
DOMAIN 39 88	HYPERVARIABLE STALK REGION.			
DOMAIN 89 470	HEAD OF NEURAMINIDASE.			
ACT_SITE 273 273	BY SIMILARITY.			
FT CARBOHYD 46 46	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 54 54	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 144 144	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 293 293	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 398 398	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 470 AA;	52015 MW; E1C1D3E2C650B93C CRC64;			
Query Match				
Best Local Similarity 100.0%; Pred. No. 70;				
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ADWSW 5			
Dd	453 ADMSW 457			
RESULT 2				
ID	NRAM_IADCH	STANDARD;	PRT;	470 AA.
AC	Q07571;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuraminidase (EC 3.2.1.18).			
GN	NA.			
OS	Influenza A virus (strain A/Duck/Hokkaido/8/80).			
OC	Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;			
OC	Influenza A viruses; Influenzavirus A.			
OX	NCBI_TaxID=38957;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93212520; PubMed=8460490;			
RA	Saito T., Kawaoka Y., Webster R.G.;			
RT	"Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";			
RL	Virology 193:868-876(1993).			
CC	- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitate the mobility of the virus to and from the site of infection.			
CC	- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.			
CC	- SUBUNIT: Homotetramer.			
CC	- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.			
CC	- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.			
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EMBL; L06573; AAA43367.1; -.				
HSSP; P06820; 2BAT.				
InterPro; IPR001860; Glyco_hydro_34.				
Pfam; PF00064; neur; 1.				
ProDom; PD000431; Glyco_hydro_34; 1.				
TRANSMEM 7 38	ANCHOR (BY SIMILARITY).			
DOMAIN 39 88	HYPERVARIABLE STALK REGION.			
DOMAIN 89 470	HEAD OF NEURAMINIDASE.			
ACT_SITE 273 273	BY SIMILARITY.			
FT CARBOHYD 46 46	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 54 54	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 144 144	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 293 293	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 398 398	N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT CARBOHYD 470 AA;	52015 MW; E1C1D3E2C650B93C CRC64;			

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 453 ADWSW 457

RESULT 4
NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; L06575; AAA43404.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F59FE364C1F49 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 453 ADWSW 457

RESULT 5
NRAM_IADU3 STANDARD; PRT; 470 AA.
AC Q07599;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; L06576; AAA16234.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 37 ANCHOR (BY SIMILARITY).
FT DOMAIN 38 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 273 PROBABLE.
FT ACT_SITE 275 275 PROBABLE.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 453 ADWSW 457

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RESULT 6
NRAM_IAGFN STANDARD; PRT; 470 AA.
ID Q07574;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
virus".
RL Virology 193:868-876 (1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
CC EMBL; L06584; AAA43428.1; -.
CC HSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 7
NRAM_IAGHD STANDARD; PRT; 470 AA.
ID Q07577;

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DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoaka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
virus".
RL Virology 193:868-876 (1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L06585; AAA43368.1; -.
CC HSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539E7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 8
NRAM_IAHJI STANDARD; PRT; 470 AA.
ID Q07578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).

```

GN NA
OS Influenza A virus (strain A/Equine/Jilinin/1/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
DR EMBL; L06579; AAA43374.1; -;
DR HSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 453 ADWSW 457
RESULT 9
NRAM IAMAE STANDARD; PRT; 470 AA.
AC Q07583;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Wallard/Edmonton/220/90).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.

OX NCBI_TaxID=38965;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
DR EMBL; L06586; AAA43369.1; -;
DR HSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 53070 MW; 557630C3E11F2765 CRC64;
Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 453 ADWSW 457
RESULT 10
NRAM IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;

RA Saito T., Kawao Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses";
CC 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
CC EMBL; L06588; AAA43410.1; -;
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT SITE 273 275 BY SIMILARITY.
FT ACT SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457
|||||
PGLR_PENGR STANDARD; PRT; 598 AA.
AC MRJ5 APIME
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 7460;
RT "Cloning and characterization of a gene encoding the
RT submitted galacturonase of Penicillium griseoroseum";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC J. Mol. Evol. 49:290-297(1999).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -1- SIMILARITY: Belongs to the major royal jelly protein family.
CC
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CC
CC EMBL; AF004842; AAD01205.1; -;
CC InterPro; IPR003534; RoyalJelly.
CC Pfam; PF03022; MRJP; 2.
CC PRINTS; PR01366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein. POTENTIAL.
FT SIGNAL 1 17
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C77E7ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 113 DMSWA 117
|||||
PGLR_PENGR STANDARD; PRT; 376 AA.
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polyalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1.
OS Penicillium griseoroseum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 6421;
RT "Cloning and characterization of a gene encoding the
RT submitted galacturonase of Penicillium griseoroseum";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
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CC

RA Saito T., Kawao Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL viruses";
CC 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitates
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
CC EMBL; L06588; AAA43410.1; -;
CC HSSP; P06820; 2BAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT SITE 273 275 BY SIMILARITY.
FT ACT SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABFF1E6B CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457
|||||
PGLR_PENGR STANDARD; PRT; 598 AA.
AC MRJ5 APIME
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 7460;
RT "Cloning and characterization of a gene encoding the
RT submitted galacturonase of Penicillium griseoroseum";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC J. Mol. Evol. 49:290-297(1999).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
CC HONEYBEE QUEEN.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
CC -1- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
CC the nurse honey bee.
CC -1- SIMILARITY: Belongs to the major royal jelly protein family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF004842; AAD01205.1; -;
CC InterPro; IPR003534; RoyalJelly.
CC Pfam; PF03022; MRJP; 2.
CC PRINTS; PR01366; ROYALJELLY.
KW Signal; Repeat; Glycoprotein. POTENTIAL.
FT SIGNAL 1 17
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C77E7ACDF63 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 113 DMSWA 117
|||||
PGLR_PENGR STANDARD; PRT; 376 AA.
AC O93883;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Polyalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).
GN PGG1.
OS Penicillium griseoroseum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=84562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCT 6421;
RT "Cloning and characterization of a gene encoding the
RT submitted galacturonase of Penicillium griseoroseum";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SIMILARITY: Belongs to family 28 of glycosyl hydrolases.
CC
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CC

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CC -----
DR EMBL; AF085238; AAC9362.1; -
DR InterPro; IPR000743; Glyco_hydro_28.
DR InterPro; IPR006626; PBH1.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR SMART; SM00710; PBH1; 5.
DR PROSITE; PS00502; POLYGALACTURONASE; 1.
KW Hydrolase; Glycosidase; Cell wall; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 376 POLYGALACTURONASE.
SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC5ED56928 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;
Best Local Similarity 66.7%; Pred. No. 1.le+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADM5WA 6
Db 349 SDMSWS 354
:||||:

RESULT 13
PAS2 SCHPO STANDARD; PRT; 1842 AA.
AC Q10289; Q14163; P78973;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [p190/210] [Includes:
DE Acyl carrier; 3-oxoacyl-[acyl-carrier protein] reductase
DE (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier
DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].
DE PAS2 OR USD1 OR SPAC4A8.11C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96354912; PubMed=8769419;
RA Saitoh S., Takahashi K., Nabeeshima K., Yamashita Y., Nakaseko Y.,
RA Hirata A., Yanagida M.;
RT "Aberrant mitosis in fission yeast mutants defective in fatty acid
RT synthetase and acetyl CoA carboxylase.";
RL J. Cell Biol. 134:949-961(1996).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/1sd1.";
RL Biochim. Biophys. Acta 1532:223-233(2001).
[3]
RP SEQUENCE FROM N.A.
RX STRAIN=972;
MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidaigo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares K., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckert G., Art R., Robben J., Grymonprez B.,
RA Weltjens I., Volckert E., Rieger M., Schaefer M., Mueller-Auer S.,

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RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzpm K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
[4]
RN SEQUENCE OF 1-215 FROM N.A.
RP Koken M.H.M., de Rooij J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[5]
RN SEQUENCE OF 1-20.
RP MEDLINE=94245730; PubMed=8188691;
RA Kaeslin E., Heyer W.-D.;
RT "Schizosaccharomyces pombe fatty acid synthase mediates DNA strand
RT exchange in vitro.";
RL J. Biol. Chem. 269:14103-14110(1994).
CC -I- FUNCTION: Fatty acid synthetase catalyzes the formation of
CC long-chain fatty acids from acetyl-CoA, malonyl-CoA and NADPH.
CC The alpha subunit contains domains for: acyl carrier protein,
CC 3-oxoacyl-[acyl-carrier protein] reductase, and 3-oxoacyl-[acyl-
CC carrier-protein] synthase. This subunit coordinates the binding
CC of the six beta subunits to the enzyme complex.
CC -I- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH = a
CC long-chain acyl-CoA + N CO(2) + 2N NADP(+).
CC -I- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-
CC carrier protein] = 3-oxoacyl-[acyl-carrier protein] + CO(2) +
CC [acyl-carrier protein].
CC -I- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
CC -I- SUBUNIT: [alpha(6)beta(6)] hexamers of two multifunctional
CC subunits (alpha and beta).
CC -I- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
CC OTHER FUNGI.
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EMBL; D83412; BAAL1913.1; -.
DR EMBL; AB013747; BAB62029.1; -.
DR EMBL; Z98762; CAB11481.1; -.
DR EMBL; U82216; AAB39943.1; -.
DR PIR; A54083; A54083.
DR PIR; T38781; T38781.
DR PIR; T43409; T43409.
DR GeneDB; SPombe; SPAC4A8.11c; -.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR004568; Pantethn_ttn.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRfam; TIGR00556; pantethn_ttn; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; 1.
DR PROSITE; PS00606; B_KETOACYL SYNTHASE; 1.
KW Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;
FT TRANSFERASE; NADP; Phosphopantetheine.
FT DOMAIN 1 ? ACYL CARRIER (ACP).
FT DOMAIN 2 ? BETA-KETOACYL REDUCTASE.

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FT DOMAIN ? 1842 BETA-KETOACYL SYNTHASE.
FT BINDING 180 180 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT ACT SITE 1262 1262 BETA-KETOACYL SYNTHASE (BY SIMILARITY).
FT CONFLICT 107 107 S -> A (IN REF. 4).
FT CONFLICT 422 422 K -> R (IN REF. 1).
SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EE571 CRC64;
Query Match 85.0%; Score 34; DB 1; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 400 SDMNA 405
RESULT 14
NOS3 SHEEP
ID_NOS3_SHEEP STANDARD; PRT; 99 AA.
AC P79209;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (BC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).
DE NOS3 OR ENOS.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RA Aguan K., Weiner C.P.;
RT Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.";
RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the NOS family.
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CC
CC EMBL; U76738; AAB40705.1; -.
CC HSSP; P29473; ID0C.
CC InterPro: IPR004030; NO_synthase.
CC Pfam; PF02898; NO_synthase; 1.
CC PROSITE; PS60001; NOS; PARTIAL.
CC Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.
FT NON_TER 1 1
FT NON_TER 99 99

SQ SEQUENCE 99 AA; 11034 MW; 82C3C765557031DA CRC64;
Query Match 82.5%; Score 33; DB 1; Length 99;
Best Local Similarity 80.0%; Pred. No. 48;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 65 ADMAW 69
RESULT 15
Y132 METJA STANDARD; PRT; 220 AA.
ID_Y132_METJA
AC Q57596;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0132.
GN MJ0132.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sult G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: TO M.JANNASCHII MJ1220 AND MJEC142.
CC -!- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).
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CC
CC EMBL; U67470; AAB98113.1; -.
CC PIR; D64316; D64316.
CC TIGR; MJ0132; -.
CC InterPro: IPR003356; N6_DNA_Mtase.
CC Pfam; PF02384; N6_Mtase; 1.
CC Hypothetical protein; Complete proteome.
SQ SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 220;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 33 ADMAW 37
RESULT 16
C1B3 SHEEP
ID_C1B3_SHEEP STANDARD; PRT; 232 AA.
AC P80943;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD1b-3 (CD1b-3 antigen) (SCD1T10)
DE (Fragment)
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal thymocytes;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RT "The sheep CD1 gene family contains at least four CD1B homologues.";
RL Immunogenetics 44:86-96(1996).
RN [2]
RP SEQUENCE OF 21-33.
RX MEDLINE=99115506; PubMed=9914336;
RA Rhind S.M., Hopkins J., Dutia B.M.;
RT "Amino-terminal sequencing of sheep CD1 antigens and identification of
a sheep CD1D gene.";
RL Immunogenetics 49:225-230(1999).
CC -1- FUNCTION: Not known.
CC -1- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X90567; CAA62187.1; -.
DR PIR; S58353; S58353.
DR HSP; P11609; 1CD1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Glycoprotein; Signal; Transmembrane; Multigene family.
FT NON TER 1 201
FT DOMAIN <1 201 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 202 222 POTENTIAL.
FT DOMAIN 223 232 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 84 194 IG-LIKE.
FT DISULFID 19 83 BY SIMILARITY.
FT DISULFID 123 178 BY SIMILARITY.
FT CARBOHYD 45 45 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 232 AA; 26023 MW; C96DB93840B56158 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 232;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
DB 156 ADWTW 160
RESULT 17
C1B2_SHEEP
ID_C1B2_SHEEP STANDARD; PRT; 333 AA.
AC Q29422;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD1b-2 precursor (CD1b-2 antigen)
DE (SCD1B-42) (Antigen IAH-CC14).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]

RP SEQUENCE FROM N.A.
RC TISSUE=thymus;
RX MEDLINE=96269982; PubMed=8662069;
RA Ferguson E.E., Dutia B.M., Hein W.R., Hopkins J.;
RT "The sheep CD1 gene family contains at least four CD1B homologues.";
RL Immunogenetics 44:86-96(1996).
RN [2]
RP SEQUENCE OF 21-33.
RX MEDLINE=99115506; PubMed=9914336;
RA Rhind S.M., Hopkins J., Dutia B.M.;
RT "Amino-terminal sequencing of sheep CD1 antigens and identification of
a sheep CD1D gene.";
RL Immunogenetics 49:225-230(1999).
CC -1- FUNCTION: Not known.
CC -1- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC -----
DR EMBL; Z36891; CAA85360.1; -.
DR PIR; S47246; S47246.
DR HSP; P11609; 1CD1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; Igc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Glycoprotein; Signal; Transmembrane; Multigene family.
FT SIGNAL 1 20
FT CHAIN 21 333 T-CELL SURFACE GLYCOPROTEIN CD1B-2.
FT DOMAIN 21 302 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 303 323 POTENTIAL.
FT DOMAIN 324 333 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 185 295 IG-LIKE.
FT DISULFID 120 184 BY SIMILARITY.
FT DISULFID 224 279 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 333 AA; 37039 MW; 861BAE9617DB9BA1 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 333;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
DB 257 ADWTW 261
RESULT 18
Y801_DEIRA
ID_Y801_DEIRA STANDARD; PRT; 410 AA.
AC Q9RW68;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative carotenoid cyclase DR0801.
GN DR0801.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RA MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1.", 1571-1577(1999).
RL Science 286:1571-1577(1999).
CC -!- SIMILARITY: Belongs to the lycopene cyclase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE001934; AAF10377.1; -.
DR PIR; D75475; D75475.
DR TIGR; DR0801; -.
DR InterPro; IPR008671; Lycopene_cycl.
DR Pfam; PF05834; Lycopene_cycl; 1.
DR PRINTS; PR00420; RINGNOXGNASE.
DR KW Hypothetical protein; Oxidoreductase; NAD; Carotenoid biosynthesis;
KW Complete proteome.
FT NP_BIND 11 39 NAD (POTENTIAL).
SQ SEQUENCE 410 AA; 43161 MW; E1B3162F10F956AF CRC64;
Query Match 82.5%; Score 33; DB 1; Length 410;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 102 ADMTW 106
RESULT 19
ID FNKL SCHPO STANDARD; PRT; 421 AA.
AC O13911;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bifunctional polynucleotide phosphatase/kinase [Includes:
DE Polynucleotide 3'-phosphatase (EC 3.1.3.32) (2'-(3')-polynucleotidase);
DE Polynucleotide 5'-hydroxyl-kinase (EC 2.7.1.78)].
GN PNK1 OR SPAC23C11.04C.
OS Schizosaccharomyces pombe (Pission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RX [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=21683566; PubMed=11729194;
RA Meijer M., Karimi-Busheri F., Huang T.Y., Weinfeld M., Young D.;
RT "Pnk1, a DNA kinase/phosphatase required for normal response to DNA
RT damage by gamma-radiation or camptothecin in Schizosaccharomyces
RT pombe.",
RL J. Biol. Chem. 277:4050-4055(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howard S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Babel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Gorym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadiou E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe".
RL Nature 415:871-880(2002).
CC -!- FUNCTION: Has a role in the repair of breaks in single stranded
CC DNA.
CC -!- CATALYTIC ACTIVITY: 3'-phosphopolynucleotide + H(2)O =
CC polynucleotide + phosphate.
CC -!- CATALYTIC ACTIVITY: ATP + 5'-dephospho-DNA = ADP + 5'-phospho-DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear
CC -!- SIMILARITY: TO HUMAN PNKP, C.ELEGANS F21D5.5, YEAST YMR156C AND
CC ACNRPV ORF33.
CC -----
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CC -----
CC EMBL; Z98559; CAB11157.1; -.
DR PIR; T38242; T38242.
DR GeneDB SPombe; SPAC23C11.04C; -.
DR InterPro; IPR006551; DNA-3-Phase.
DR TIGR; TIGR01664; DNA-3-Phase.
DR TIGRFAMs; TIGR01664; DNA-3-Phase; 1.
DR TIGRFAMs; TIGR01662; HAD-SF-IIIa; 1.
DR Multifunctional enzyme; Transferase; Kinase; Hydrolase; DNA repair;
KW ATP-binding; Nuclear protein. ATP (POTENTIAL).
FT NP_BIND 263 270
SQ SEQUENCE 421 AA; 48477 MW; FE9A732CD40E3146 CRC64;
Query Match 82.5%; Score 33; DB 1; Length 421;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 93 ADMTW 97
RESULT 20
ID NRAW IAQIT STANDARD; PRT; 470 AA.
AC Q07584;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Quail/Italy/1117/65).

Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 Influenza A viruses; Influenzavirus A.
 NCBI_TaxID=38976;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=93212520; PubMed=8460490;
 Saito T., Kawaoka Y., Webster R.G.;
 "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
 viruses";
 Virology 193:868-876(1993).
 -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 chains of the host cell surface proteins and from the viral
 envelope. Such a reaction prevents self-aggregation and facilitate
 the mobility of the virus to and from the site of infection.
 -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 oligosaccharides, glycoproteins, glycolipids, colominic acid and
 synthetic substrates.
 -1- SUBUNIT: Homotrimer.
 -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
 spike on the surface of the virion.
 -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
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 EMBL; L06587; AAA3373.1; -;
 HSP; P06820; 2BAT.
 InterPro; IPR001860; Glyco_hydro_34.
 Pfam; PF00064; neu; 1.
 ProDom; PD000431; Glyco_hydro_34; 1.
 Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
 TRANSMEM 7 38
 DOMAIN 39 88
 ACT SITE 273 273
 ACT_SITE 275 275
 CARBOHYD 46 46
 CARBOHYD 54 54
 CARBOHYD 84 84
 CARBOHYD 144 144
 CARBOHYD 293 293
 CARBOHYD 398 398
 SEQUENCE 470 AA; 52005 MW; 9F743833EAC7F1C2 CRC64;
 Query Match 82.5%; Score 33; DB 1; Length 470;
 Best Local Similarity 80.0%; Pred. No. 2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ADWSW 5
 Db 453 ADWTW 457
 RESULT 21
 BGLA_BACSU
 ID BGLA_BACSU STANDARD; PRT; 479 AA.
 AC P42973;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 6-phospho-beta-glucosidase (EC 3.2.1.86).
 GN BGLA OR BSU4010.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=168 / JH642;
 RA MEDLINE=94171085; PubMed=8125345;
 RX Zhang J., Aronson A.I.;
 RT "A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is
 RT inducible and closely linked to a NADH dehydrogenase-encoding gene.";
 RL Gene 140:85-90(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
 RT "36kb sequence between gntz and trnY of B. subtilis genome.";
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 Azevedo V., Betero M.G., Bessieres P., Bolotin A., Borchert S.,
 Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerth I.F., Cummings N.J., Daniel R.A.,
 Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 Guiseppe H., Guy B.J., Haga K., Hache J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.P., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone P.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 Viari A., Wambut R., Wedler E., Wedler H., Weitzneger T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis";
 Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: 6-phospho-beta-D-glucoside-(1,4)-D-glucose +
 H(2)O = D-glucose 6-phosphate + D-glucose.
 CC -1- SIMILARITY: Belongs to family 1 of glycosyl hydrolases.
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 EMBL; L19710; AAA22660.1; -;
 EMBL; D78193; BAA11270.1; -;
 EMBL; Z99124; CAB6048.1; -;
 PIR; I39953; I39953.
 HSP; P11546; 1PBG.
 Subtilist; BG11203; bglA.
 InterPro; IPR001360; Glyco_hydro_1.
 Pfam; PF00222; Glyco_hydro_1_1.
 PRINTS; PR00131; GLHYDRLASE1.
 ProDom; PD000650; Glyco_hydro_1; 1.
 PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 1.
 PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 1.
 Hydrolase; Glycosidase; Complete Proteome.
 ACT_SITE 176 176 PROTON DONOR (POTENTIAL).
 FT

Matches 4; Conservative 1; Mismatches 0; Gaps 0

2 DWSWA 6
|||:
395 DWNWA 399

RESULT 23

GUAU_MYCLE

GUAA_MYCLE STANDARD; PRT; 529 AA.

P46810; Q9CCU9;
01-NOV-1995 (rel. 32, Created)
DT 28-FEB-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (Glutamine
DE amidotransferase) (GMP synthetase).
DE GUAA OR ML0395 OR B1620_C2_205.
GN Mycobacterium leprae.
OS Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1769;
[1]
SEQUENCE FROM N.A.
RA Smith D.R., Robison K.;
RA Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
RRL [2]
SEQUENCE FROM N.A.
RP STRAIN=TN;
RC MEDLINE=21128732; PubMed=11234002;
RX Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Rajadream M.A., Maclean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Raftery J., Rutherford K.W.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RA "Massive gene decay in the leprosy bacillus";
RL Nature 409:1007-1011(2001).
RT -! CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +
CC -! H(2)O = AMP + diphosphate + GMP + L-glutamate.
CC -! PATHWAY: GMP biosynthesis.
CC -! SUBUNIT: Homodimer (By similarity).
CC -! SIMILARITY: In the C-terminal section; belongs to the GMP synthase
CC family.
CC -! SIMILARITY: Contains 1 type-1 glutamine amidotransferase domain.

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EMBL; U00015; AAC3222.1; ALT INIT.
DR EMBL; AL583918; CAC29903.1; -
DR FJX; C86958; C86958.
DR HSP; P04079; IGFM.
DR Leptoma; ML0395; -.
DR HAMAP; MF 00344; -. 1.
DR InterPro; IPRO06220; Anth_synthII.
DR InterPro; IPRO01317; CP synthGatase.
DR InterPro; IPRO00991; Gatase 1.
DR InterPro; IPRO01674; GMP_synth_C.
DR InterPro; IPRO04739; GMP_synth_N.
DR Pfam; PF00117; Gatase; 1.
DR Pfam; PF00958; GMP_synt_C; 1.
DR PRINTS; PR00097; ANTSNTHASE1I.
DR PRINTS; PR00099; CPGATASE.
DR PRINTS; PR00096; GATASE.
DR TIGRFAMs; TIGR00884; guaA_Cterm; 1.

```
DR TIGRPMs; TIGR00888; gaaA_Nterm; 1.
DR PROSITE; PS00442; GATASE_TYPE 1; 1.
KW Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
KW Glutamine amidotransferase; Complete proteome.
FT DOMAIN 1 204 GLUTAMINE AMIDOTRANSFERASE.
FT DOMAIN 237 404 GMP-BINDING (BY SIMILARITY).
FT ACT_SITE 93 93 GATASE (BY SIMILARITY).
FT ACT_SITE 179 179 GATASE (BY SIMILARITY).
FT ACT_SITE 181 181 GATASE (BY SIMILARITY).
FT NP_BIND 233 239 ATP (BY SIMILARITY).
SQ SEQUENCE 529 AA; 56723 MW; 443EDE9525CDD949 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 529;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 487 ADWTW 491

RESULT 24
YC20_METJA STANDARD; PRT; 578 AA.
AC Q58617;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ1220.
GN MJ1220.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervilave A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii.";
RL Science 273:1058-1073(1996).
CC -1- SIMILARITY: TO M.JANNASCHII MJ0132 AND MJEL42.
CC -1- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES
CC (M SUBUNIT).
CC -----
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CC -----
DR EMBL; U67563; AAB99225.1; -.
DR EMBL; C64452; C64452.
DR TIGR; MJ1220; -.
DR InterPro; IPR003665; Methylase M.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR003356; N6_DNA_Mcase.
DR InterPro; IPR002052; N6_Mcase.
DR Pfam; PF02506; Methylase M; 1.
DR Pfam; PF02384; N6_Mcase; 1.
DR PRINTS; PR00507; N12N6MTFASER.
DR PROSITE; PS00092; N6_MTASE; 1.
KW Hypothetical protein; Complete proteome.
```

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SQ SEQUENCE 578 AA; 66636 MW; 5339ED873EF8E9E2 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 578;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 391 ADWAW 395

RESULT 25
YC12_KLEPN STANDARD; PRT; 579 AA.
AC Q48458;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 65.4 kDa protein in cps region (ORF12).
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Chedid;
RX MEDLINE=95204345; PubMed=7896702;
RA Arakawa Y., Wacharotayankun R., Nagatsuka T., Ito H., Kato N.,
RA Ohta M.;
RT "Genomic organization of the Klebsiella pneumoniae cps region
RT responsible for serotype K2 capsular polysaccharide synthesis in the
RT virulent strain Chedid.";
RL J. Bacteriol. 177:1788-1796(1995).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D21242; BAA04783.1; -.
DR KW Hypothetical protein.
SQ SEQUENCE 579 AA; 65385 MW; 7A8994B7590202DE CRC64;

Query Match 82.5%; Score 33; DB 1; Length 579;
Best Local Similarity 80.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 537 SDWSW 541

RESULT 26
PHK_STRCO STANDARD; PRT; 817 AA.
AC Q8CK51;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable phosphotolase (EC 4.1.2.-).
GN SCO0617 OR SCF56.01C OR SCF55.41C.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
```

```

CC reducing ends of the chains.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY L (FAMILY 48 OF GLYCOSYL
CC HYDROLASES).
CC -----
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CC -----
CC EMBL; Z69359; CAA93280.1; -.
CC HSSP; Q06851; LNCC.
CC InterPro; IPR001956; CBD_3.
CC InterPro; IPR008965; Cellul_bind.
CC InterPro; IPR005102; DUF291.
CC InterPro; IPR000556; Glyco_hydro_48.
CC InterPro; IPR008928; Glyco_trans_6hp.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00942; CBM_3; 1.
CC Pfam; PF03442; DUF291; 1.
CC Pfam; PF02011; Glyco_hydro_48; 1.
CC PRINTS; PR00844; GLHYDRLASE48.
CC ProDom; PD011947; CBD_3; 1.
CC ProDom; PD011903; Glyco_hydro_48; 1.
CC Cellulose degradation; Hydrolase; Glycosidase; signal.
CC SIGNAL 1
CC CHAIN 34 914
CC SEQUENCE 914 AA; 103020 MW; D0DB6017D6DF82C CRC64;
CC -----
CC Query Match 82.5%; Score 33; DB 1; Length 914;
CC Best Local Similarity 80.0%; Pred. No. 3.7e+02;
CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC -----
CC Qy 1 ADWSW 5
CC |||||
CC 338 ADWAW 342
CC Db

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ID	NOS3 MOUSE	STANDARD;	PRT;	1201 AA.
AC	P703T3;	O55056;		
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type			
DE	III) (NOSIII) (endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).			
GN	NOS OR ECNOS.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal heart;			
RX	MEDLINE=96350460; PubMed=8764825;			
RA	Gnanapandithen K., Chen Z., Kau C.-L., Gorczynski R.M., Marsden P.A.;			
RT	"Cloning and characterization of murine endothelial constitutive			
RT	nitric oxide synthase.";			
RL	Biochim. Biophys. Acta 1308:103-106(1996).			
[2]				
RN	SEQUENCE OF 1-53 FROM N.A.			
RC	TISSUE=Fetal heart;			
RA	Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.L., O'Brien W.E.;			
RT	"limb reduction defects in endothelial nitric oxide synthase deficient			
RT	mice.";			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
[3]				
RN	FUNCTION.			
RP	MEDLINE=99061722; PubMed=9843834;			
RX	Gregg A.R., Schauer A., Shi O., Liu Z., Lee C.G.L., O'Brien W.B.;			

RT "Limb reduction defects in endothelial nitric oxide synthase-deficient
RL mice."; Physiol. 275:H2319-H2324(1998).
CC -1- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets. May
CC play a significant role in normal and abnormal limb development.
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -1- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -1- ENZYME REGULATION: Stimulated by calcium/calmodulin (By
CC similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the NOS family.
CC -1- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC -----
DR EMBL; U53142; AAC52766.1; -;
DR EMBL; AF045940; AAC02553.1; -;
DR PIR; S71424; S71424.
DR HSP; P29474; 3NOS.
DR MGD; MGI:97362; Nos3.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxid FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Myristate;
KW Lipoprotein; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
KW Multigene family.
FT INIT MET 0
FT DOMAIN 518 701
FT METAL 182 182
FT DOMAIN 489 508
FT NP_BIND 647 678
FT NP_BIND 791 802
FT NP_BIND 933 943
FT NP_BIND 1008 1026
FT NP_BIND 1106 1121
FT LIPID 1
FT LIPID 14 14
FT LIPID 25 25
FT METAL 92 92
FT METAL 97 97
FT CONFLICT 49 49
SQ SEQUENCE 1201 AA; 132748 MW; DA37ABAC947DABD5 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 1201;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWAW 5
|||:

Db 441 ADWAW 445
RESULT 29
NOS3 HUMAN
ID NOS3_HUMAN STANDARD; PRT; 1202 AA.
AC P29474; Q13662; Q14251; Q14434;
DT 01-APR-1993 (Rel. 25, Created)
DT 15-JUL-1993 (Rel. 26, Last sequence update)
DT 01-MAR-2004 (Rel. 43, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92340475; PubMed=1378832;
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RT "Cloning and expression of a cDNA encoding human endothelium-derived
RT relaxing factor/nitric oxide synthase";
RL J. Biol. Chem. 267:14519-14522(1992).
RN [2]
RP ERRATUM.
RA Janssens S.P., Shimouchi A., Quertermous T., Bloch D.B., Bloch K.D.;
RL J. Biol. Chem. 267:22694-22694(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92354731; PubMed=1379542;
RA Marsden P.A., Schappert K.T., Chen H.S., Flowers M., Sundell C.L.,
RA Wilcox J.N., Lamas S., Michel T.;
RT "Molecular cloning and characterization of human endothelial nitric
RT oxide synthase";
RL FEBS Lett. 307:287-293(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93352539; PubMed=7688726;
RA Marsden P.A., Heng H.H., Scherer S.W., Stewart R.J., Hall A.V.,
RA Shi X.-M., Tsui L.-C., Schappert K.T.;
RT "Structure and chromosomal localization of the human constitutive
RT endothelial nitric oxide synthase gene";
RL J. Biol. Chem. 268:17478-17488(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Liao J.K.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94161710; PubMed=7509596;
RA Nadaud S.A., Bonnardaux A., Lathrop M., Soubrier F.;
RT "Gene structure, polymorphism and mapping of the human endothelial
RT nitric oxide synthase gene";
RL Biochem. Biophys. Res. Commun. 198:1027-1033(1994).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=94333373; PubMed=7519987;
RA Miyahara K., Kawamoto T., Sase K., Yui Y., Toda K., Yang L.X.,
RA Hattori R., Aoyama T., Yamamoto Y., Doi Y., Ogoshi S.,
RA Hashimoto K., Kawai C., Sasayama S., Shizuta Y.;
RT "Cloning and structural characterization of the human endothelial
RT nitric-oxide-synthase gene";
RL Eur. J. Biochem. 223:719-726(1994).
RN [8]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuidanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE OF 1-52 FROM N.A.

RC TISSUE=Placenta;
RX MEDLINE=94245207; PubMed=7514568;
RA Robinson L.J., Werenowicz S., Morton C.C., Michel T.;
RT "Isolation and chromosomal localization of the human endothelial
RL nitric oxide synthase (NOS3) gene.";
RL Genomics 19:350-357(1994).
[10]
RP SEQUENCE OF 410-527 FROM N.A.
RC TISSUE=Platelet;
RX MEDLINE=96077182; PubMed=7475956;
RA Sase K., Michel T.;
RT "Expression of constitutive endothelial nitric oxide synthase in human
RL blood platelets.";
RL Life Sci. 57:2049-2055(1995).
[11]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=99173237; PubMed=10074942;
RA Fischmann T.O., Hruza A., Niu X.D., Fossetta J.D., Lunn C.A.,
RA Dolphin E., Prongay A.J., Reichert P., Lundell D.J., Narula S.K.,
RA Weber P.C.;
RT "Structural characterization of nitric oxide synthase isoforms
RT reveals striking active-site conservation.";
RL Nat. Struct. Biol. 6:233-242(1999).
[12]
RP X-RAY CRYSTALLOGRAPHY (1.96 ANGSTROMS) OF 66-479.
RX MEDLINE=22325496; PubMed=12437348;
RA Rosenfeld R.J., Garcia E.D., Panda K., Andersson G., Aberg A.,
RA Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,
RA Getzoff E.D.;
RT "Conformational changes in nitric oxide synthases induced by
RT chlorzoxazone and nitroindazoles: crystallographic and computational
RT analyses of inhibitor potency.";
RL Biochemistry 41:13915-13925(2002).
[13]
RP VARIANT SUSCEPTIBILITY TO CORONARY SPASM ASP-297.
RX MEDLINE=98407797; PubMed=9737779;
RA Yoshimura M., Yasue H., Nakayama M., Shimazaki Y., Sumida H.,
RA Sugiyama S., Kugiyama K., Ogawa H., Saito Y., Miyamoto Y.,
RA Nakao K.;
RT "A missense Glu298Asp variant in the endothelial nitric oxide synthase
RT gene is associated with coronary spasm in the Japanese.";
RL Hum. Genet. 103:65-69(1998).
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets.
CC -!- CATALYTIC ACTIVITY: L-arginine + NADPH + H⁺ = citrulline +
CC nitric oxide + NADP(+).
CC -!- COPACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: Platelets.
CC -!- POLYMORPHISM: Variation in NOS3 seem to be associated with
CC susceptibility to coronary spasm.
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.

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DR EMBL; M93718; AAA36364.1; -;
DR EMBL; M95296; AAA36372.1; -;
DR EMBL; L10709; AAA36365.1; -;
DR EMBL; L10693; AAA36365.1; JOINED.
DR EMBL; L10694; AAA36365.1; JOINED.

DR EMBL; L10695; AAA36365.1; JOINED.
DR EMBL; L10696; AAA36365.1; JOINED.
DR EMBL; L10697; AAA36365.1; JOINED.
DR EMBL; L10698; AAA36365.1; JOINED.
DR EMBL; L10699; AAA36385.1; JOINED.
DR EMBL; L10700; AAA36385.1; JOINED.
DR EMBL; L10701; AAA36365.1; JOINED.
DR EMBL; L10702; AAA36365.1; JOINED.
DR EMBL; L10703; AAA36365.1; JOINED.
DR EMBL; L10704; AAA36365.1; JOINED.
DR EMBL; L10705; AAA36385.1; JOINED.
DR EMBL; L10706; AAA36385.1; JOINED.
DR EMBL; L10707; AAA36365.1; JOINED.
DR EMBL; L10708; AAA36365.1; JOINED.
DR EMBL; L26914; AAA36374.1; -;
DR EMBL; X76303; CAA53950.1; -;
DR EMBL; X76304; CAA53950.1; JOINED.
DR EMBL; X76305; CAA53950.1; JOINED.
DR EMBL; X76306; CAA53950.1; JOINED.
DR EMBL; X76307; CAA53950.1; JOINED.
DR EMBL; X76308; CAA53950.1; JOINED.
DR EMBL; X76309; CAA53950.1; JOINED.
DR EMBL; X76310; CAA53950.1; JOINED.
DR EMBL; X76311; CAA53950.1; JOINED.
DR EMBL; X76312; CAA53950.1; JOINED.
DR EMBL; X76313; CAA53950.1; JOINED.
DR EMBL; X76314; CAA53950.1; JOINED.
DR EMBL; X76315; CAA53950.1; JOINED.
DR EMBL; X76316; CAA53950.1; JOINED.
DR EMBL; D26607; BAA05652.1; -;
DR EMBL; AF519768; AAM74944.1; -;
DR EMBL; L23210; AAA36373.1; -;
DR EMBL; S80791; AAD14336.1; -;
DR PIR; A47501; A47501.
DR PDB; 3NOS; 04-FEB-00.
DR PDB; 1M9J; 11-DEC-02.
DR PDB; 1M9K; 11-DEC-02.
DR PDB; 1M9N; 11-DEC-02.
DR PDB; 1M9Q; 11-DEC-02.
DR PDB; 1M9R; 11-DEC-02.
DR Genew; HGNC:7876; NOS3.
DR MTM; 163729; -;
DR GO; GO:0005737; Cytoplasm; TAS.
DR GO; GO:0004517; Finitric-oxide synthase activity; TAS.
DR GO; GO:0006928; P-cell motility; TAS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN_cyt_redctase.
DR InterPro; IPR004030; NO_synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; PFNCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.

Query Match 82.58; Score 33; DB 1; Length 1202;
Best Local Similarity 80.08; Pred.No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADMSW 5
Db 442 ADMAW 446

RESULT 30
NOS3_BOVIN
ID_NOS3_BOVIN STANDARD; PRT; 1204 AA.
AC P29473;

DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92335295; PubMed=1378626;
RX Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
RA "Endothelial nitric oxide synthase: molecular cloning and
RT characterization of a distinct constitutive enzyme isoform";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=93055452; PubMed=1385480;
RX Nishida K., Harrison D.G., Navas J.P., Fisher A.A., Dockery S.P.,
RA Uematsu M., Nerem R.M., Alexander R.W., Murphy T.J.;
RA "Molecular cloning and characterization of the constitutive bovine
RT aortic endothelial cell nitric oxide synthase";
RL J. Clin. Invest. 90:2092-2096(1992).
RN [3]
RN SEQUENCE FROM N.A.
RP TISSUE=Aortic endothelium;
RX MEDLINE=92348367; PubMed=1379225;
RA Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,
RA D'Angelo D.D., Lynch K.R., Peach M.J.;
RA "Molecular cloning and expression of a cDNA encoding endothelial cell
RT nitric oxide synthase";
RL J. Biol. Chem. 267:15274-15276(1992).
RN [4]
RN MYRISTOYLATION.
RP MEDLINE=93231982; PubMed=7682550;
RX Busconi L., Michel T.;
RA "Endothelial nitric oxide synthase. N-terminal myristoylation
RT determines subcellular localization.";
RL J. Biol. Chem. 268:8410-8413(1993).
RN [5]
RN PALMITOYLATION.
RP MEDLINE=96102197; PubMed=8524847;
RX Robinson L.J., Michel T.;
RA "Mutagenesis of palmitoylation sites in endothelial nitric oxide
RT synthase identifies a novel motif for dual acylation and subcellular
RT targeting";
RL Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).
RN [6]
RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.
RP MEDLINE=99091052; PubMed=9875848;
RX Raman C.S., Li H., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
RA "Crystal structure of constitutive endothelial nitric oxide synthase:
RT a paradigm for pterin function involving a novel metal center.";
RL Cell 95:939-950(1998).
RN [7]
RN X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS) OF 66-481.
RX MEDLINE=20503854; PubMed=11051558;
RA Li H., Raman C.S., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
RA "Mapping the active site polarity in structures of endothelial
RT nitric oxide synthase heme domain complexed with isothioureas.";
RL J. Inorg. Biochem. 81:133-139(2000).
RN [8]
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).
RX MEDLINE=21229525; PubMed=11331003;
RA Li H., Raman C.S., Martasek P., Masters B.S.S., Poulos T.L.;
RA "Crystallographic studies on endothelial nitric oxide synthase
RT complexed with nitric oxide and mechanism-based inhibitors";
RL Biochemistry 40:5399-5406(2001).
RN [9]
RN X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
RX MEDLINE=21552923; PubMed=11695891;
RX Raman C.S., Li H., Martasek P., Southan G., Masters B.S.S.,
RA Poulos T.L.;
RA "Crystal structure of nitric oxide synthase bound to nitro indazole
RT reveals a novel inactivation mechanism";
RL Biochemistry 40:13448-13455(2001).
RN [10]
RN X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).
RX MEDLINE=21336567; PubMed=11331290;
RX Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,
RA Masters B.S.S., Poulos T.L.;
RA "Implications for isoform-selective inhibitor design derived from the
RT binding mode of bulky isothioureas to the heme domain of endothelial
RT nitric-oxide synthase";
RL J. Biol. Chem. 276:26486-26491(2001).
RN [11]
RN X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS).
RX MEDLINE=21623579; PubMed=11590164;
RX Kotsonis P., Frohlich L.G., Raman C.S., Li H., Berg M., Gerwig R.,
RA Groehn V., Kang Y., Al-Masoudi N., Taghavi-Moghadam S., Mohr D.,
RA Munch U., Schnabel J., Martasek P., Masters B.S.S., Strobel H.,
RA Poulos T., Matter H., Pfeleiderer W., Schmidt H.H.W.;
RA "Structural basis for pterin antagonism in nitric-oxide synthase.
RT Development of novel 4-oxo-pteridine antagonists of
RT (8R)-5,6,7,8-tetrahydrobiopterin";
RL J. Biol. Chem. 276:49133-49141(2001).
RN [12]
RN FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets.
CC -I- CATALYTIC ACTIVITY: L-arginine + NADPH + H⁺ = citrulline +
CC nitric oxide + NADP(+).
CC -I- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme.
CC -I- ENZYME REGULATION: Stimulated by calcium/calmodulin.
CC -I- SUBUNIT: Homodimer.
CC -I- SIMILARITY: Belongs to the NOS family.
CC -I- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M99057; AAA30667.1; -;
DR EMBL; M89952; AAA30494.1; -;
DR EMBL; M95674; AAA30669.1; -;
DR PIR; A38943; A38943.
DR PDB; 1NSE; 18-MAY-99.
DR PDB; 2NSE; 25-MAY-99.
DR PDB; 3NSE; 18-MAY-99.
DR PDB; 4NSE; 18-MAY-99.
DR PDB; 8NSE; 21-NOV-01.
DR PDB; 9NSE; 25-OCT-00.
DR PDB; 1D1W; 25-OCT-00.
DR PDB; 1ED4; 25-OCT-00.
DR PDB; 1DM6; 21-NOV-01.
DR PDB; 1DM7; 13-DEC-00.
DR PDB; 1DM8; 13-DEC-00.
DR PDB; 1DMT; 20-DEC-00.
DR PDB; 1DMJ; 04-JAN-01.
DR PDB; 1ED5; 12-DEC-01.
DR PDB; 1ED6; 08-AUG-01.
DR PDB; 1FOI; 20-JUL-01.
DR PDB; 1FOL; 20-JUL-01.
DR PDB; 1FOO; 20-JUL-01.
DR PDB; 1FOP; 20-JUL-01.
DR PDB; 1DIV; 25-JUL-01.

```
DR PDB: 1D1X; 25-JUL-01.
DR PDB: 1D1Y; 25-JUL-01.
DR PDB: 1D0C; 21-NOV-01.
DR PDB: 1D00; 21-NOV-01.
DR PDB: 1FOJ; 16-NOV-01.
DR PDB: 1DMK; 04-JAN-02.
DR PDB: 1I83; 08-AUG-01.
DR PDB: 5NSE; 29-MAY-02.
DR PDB: 6NSE; 23-MAY-02.
DR PDB: 7NSE; 23-MAY-02.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR001709; FPN cyt redctse.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; OxRed_FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; flavodoxin; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FENCR.
DR PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
DR PROSITE; PS60001; NOS; 1.
DR Blood coagulation; Oxidoreductase; Calcium-binding;
KW Calmodulin-binding; FAD; FMN; Heme; Metal-binding; NADP; Zinc;
KW Lipoprotein; Myristate; Palmitate; Phosphorylation; Multigene family;
KW 3D-structure.
FT INIT_MET 0 0
FT DOMAIN 521 704
FT METAL 185 185
FT DOMAIN 491 511
FT NP_BIND 650 681
FT NP_BIND 794 805
FT NP_BIND 936 946
FT NP_BIND 1011 1029
FT NP_BIND 1109 1124
FT LIPID 1 1
FT LIPID 14 14
FT LIPID 25 25
FT METAL 95 95
FT METAL 100 100
FT MOD_RES 142 142
FT CONFLICT 99 99
FT CONFLICT 164 164
FT CONFLICT 317 327
FT CONFLICT 454 454
FT CONFLICT 458 458
FT CONFLICT 740 740
FT CONFLICT 803 804
FT CONFLICT 856 856
FT CONFLICT 906 907

Query Match 82.5%; Score 33; DB 1; Length 1204;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 444 ADMAW 448

RESULT 31
NOS3_PIG
ID NOS3_PIG STANDARD; PRT; 1204 AA.
AC Q28369;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type
DE III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS).
GN NOS3 OR NOS.
OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE=Pulmonary artery;
RA MEDLINE=97293429; PubMed=9149402;
RA Zhang J., Patel J.M., Block E.R.;
RT "Molecular cloning, characterization and expression of a nitric oxide
RT synthase from porcine pulmonary artery endothelial cells.";
RL Comp. Biochem. Physiol. 116B:485-491(1997).
RN [2]
RP SEQUENCE OF 1031-1205 FROM N.A.
RA Patel J.M., Block E.R.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Produces nitric oxide (NO) which is implicated in
CC vascular smooth muscle relaxation through a cGMP-mediated signal
CC transduction pathway. No mediates vascular endothelial growth
CC factor (VEGF)-induced angiogenesis in coronary vessels and
CC promotes blood clotting through the activation of platelets (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline +
CC nitric oxide + N NADP(+).
CC -!- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (By similarity).
CC -!- ENZYME REGULATION: Stimulated by calcium/calmodulin (By
CC similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- INDUCTION: REPPRESSED BY PROINFLAMMATORY CYTOKINES.
CC -!- SIMILARITY: Belongs to the NOS family.
CC -!- SIMILARITY: Contains 1 flavodoxin-like domain.
CC -----
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CC -----
EMBL; U59924; AAB39539.1; -.
EMBL; U33832; AAB4933.1; -.
HSP; P29473; 1D0C.
InterPro; IPR003097; FAD_binding.
InterPro; IPR008254; Flav nitox synth.
InterPro; IPR001094; Flavodoxin like.
InterPro; IPR001709; FPN cyt redctse.
InterPro; IPR004030; NO synthase.
InterPro; IPR001433; OxRed_FAD/NAD(P).
Pfam; PF00667; FAD_binding_1; 1.
Pfam; PF00258; flavodoxin; 1.
Pfam; PF00175; NAD binding_1; 1.
PRINTS; PR00369; NO synthase; 1.
PRINTS; PR00371; FENCR.
PROSITE; PS50902; FLAVODOXIN_LIKE; 1.
PROSITE; PS60001; NOS; 1.
Lipoprotein; Myristate; Palmitate; Calcium-binding; Heme; Zinc; Metal-binding;
Multigene family.
INIT_MET 0 0
DOMAIN 521 704
METAL 185 185
DOMAIN 491 511
NP_BIND 650 681
NP_BIND 794 805
NP_BIND 936 946
NP_BIND 1011 1029
NP_BIND 1109 1124
LIPID 1 1
LIPID 14 14
LIPID 25 25
BY SIMILARITY.
FLAVODOXIN-LIKE.
IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CALMODULIN-BINDING (POTENTIAL).
FMN (PYRIMIDINE PART) (BY SIMILARITY).
FAD (ADP PART) (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
N-myristoyl glycine.
S-palmitoyl cysteine.
S-palmitoyl cysteine.
ZINC.
ZINC.
PHOSPHORYLATION (BY PKA).
C -> R (IN REF. 3).
Y -> I (IN REF. 3).
EHPLEWPAAL -> GAPHTGVWRGP (IN REF. 3).
S -> Y (IN REF. 3).
T -> P (IN REF. 3).
T -> A (IN REF. 3).
CP -> SA (IN REF. 3).
L -> V (IN REF. 3).
WF -> LV (IN REF. 3).
```


FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 100 100 ZINC (BY SIMILARITY).
SQ SEQUENCE 1204 AA; 133274 MW; 48676BA95D814CFE CRC64;

Query Match 82.5%; Score 33; DB 1; Length 1204;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 444 ADMAW 448

RESULT 32
NOS3 CAVPO STANDARD; PRT; 100 AA.
ID NOS3_CAVPO
AC P97270;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (BC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).
GN NOS3 OR ENOS.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial cells;
RX MEDLINE=99057793; PubMed=9838160;
RA Aguan K., Murotsuki J., Gagnon R., Thompson L.P., Weiner C.P.;
RT "Effect of chronic hypoxemia on the regulation of nitric-oxide synthase in the fetal sheep brain."
RL Brain Res. Dev. Brain Res. 111:271-277(1998).
CC -1- FUNCTION: Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cAMP-mediated signal transduction pathway. No mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets (By similarity).
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).
CC -1- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires tetrahydrobiopterin (BH4) which may stabilize the dimeric form of the enzyme (By similarity).
CC -1- ENZYME REGULATION: Stimulated by calcium/calmodulin (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- INDUCTION: Repressed by hypoxemia in fetal brain.
CC -1- SIMILARITY: Belongs to the NOS family.
CC -----
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CC -----
DR EMBL; U76736; AAB40703.1; -.
DR HSP; P29474; 3NOS.
DR InterPro; IPR004030; NO synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; PARTIAL.
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding;
KW Heme; Multigene family.
FT NON TER 1
FT NON TER 100
SQ SEQUENCE 100 AA; 11271 MW; 867D7F89F4B132A8 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 100;

Best Local Similarity 80.0%; Pred. No. 68;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 88 ADMGW 92

RESULT 33
STEL RHUVE STANDARD; PRT; 107 AA.
ID STEL_RHUVE
AC P00302;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Stellacyanin.
OS Rhus vernicifera (Japanese lacquer tree) (Varnish tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; OC eurosids II; Sapindales; Anacardiaceae; Toxicodendron.
OX NCBI_TaxID=4013;
RN [1]
RP SEQUENCE.
RX MEDLINE=77266668; PubMed=901509;
RA Bergman C., Gandvik E.K., Nyman P.O., Strid L.;
RT "The amino acid sequence of stellacyanin from the lacquer tree."
RL Biochem. Biophys. Res. Commun. 77:1052-1059(1977).
RN [2]
RP ERRATUM.
RA Bergman C., Gandvik E.K., Nyman P.O., Strid L.;
RL Biochem. Biophys. Res. Commun. 79:1013-1013(1977).
RN [3]
RX MEDLINE=84208877; PubMed=6723985;
RA Engeseth H.R., Hermanson M.A., McMillin D.R.;
RT "A new assignment of the disulfide linkage in stellacyanin."
RL FEBS Lett. 171:257-261(1984).
RN [4]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=92106330; PubMed=1762145;
RA Fields B.A., Guss J.M., Freeman H.C.;
RT "Three-dimensional model for stellacyanin, a 'blue' copper-protein."
RL J. Mol. Biol. 222:1053-1065(1991).
CC -1- FUNCTION: The midpoint redox potential is +184 mV.
CC -1- SIMILARITY: Contains 1 plastocyanin-like domain.
DR PIR; A00311; SSUL.
DR HSP; P00303; 2CBP.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR003245; Pleyanin_like.
DR Pfam; PF02298; Cu bind like; 1.
DR ProDom; PD003122; Pleyanin like; 1.
DR PROSITE; PS00196; COPPER BLUE; 1.
KW Electron transport; Copper; Glycoprotein.
FT DOMAIN 1 107 PLASTOCYANIN-LIKE.
FT DISULFID 59 93 COPPER.
FT METAL 46 46 COPPER.
FT METAL 87 87 COPPER.
FT METAL 92 92 COPPER.
FT METAL 97 97 COPPER.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .).
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .).
FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .).
SQ SEQUENCE 107 AA; 12296 MW; 4AP450E1A0461069 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 107;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 22 DAKWA 26

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Query Match 80.0%; Score 32; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSW 5
Db 35 DWSW 38

RESULT 36
3MG2_ECOLI
ID 3MG2_ECOLI STANDARD; PRT; 282 AA.
AC P04395;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-3-methyladenine glycosylase II (EC 3.2.2.21) (3-methyladenine-DNA
DE glycosylase II, inducible) (TAG II) (DNA-3-methyladenine glycosidase
DE II).
GN ALKA OR AIDA OR B2068.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
OX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-12 AND 14-20.
RP MEDLINE=85054800; PubMed=6094528;
RX Nakabeppu Y., Miyata T., Kondo H., Iwanaga S., Sekiguchi M.;
RA "Structure and expression of the alka gene of Escherichia coli
RT involved in adaptive response to alkylating agents.";
RL J. Biol. Chem. 259:13730-13736(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RA MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Ferna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RA MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sauegi G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

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Query Match 80.0%; Score 32; DB 1; Length 125;
Best Local Similarity 80.0%; Pred. No. 84;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 68 ADWEW 72

RESULT 35
CY1_RHORI
ID CY1_RHORI STANDARD; PRT; 272 AA.
AC P2335;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c1 precursor.
GN PTC.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OC NCBI_TaxID=1085;
OX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 25-50.
RP STRAIN=PR1;
RX MEDLINE=91094774; PubMed=2176269;
RA Majewski C., Trebst A.;
RT "The pet genes of Rhodospirillum rubrum: cloning and sequencing of
RL the genes for the cytochrome bcl-complex.";
RL Mol. Gen. Genet. 224:373-382(1990).
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
CC complex (complex III or cytochrome b-c1 complex), which is a
CC respiratory chain that generates an electrochemical potential
CC coupled to ATP synthesis.
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
CC cytochrome c1 and the Rieske protein.
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RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=85054799; PubMed=6389535;
RA Nakabeppu Y., Kondo H., Sekiguchi M.;
RT "Cloning and characterization of the alkA gene of Escherichia coli
RL that encodes 3-methyladenine DNA glycosylase II.";
RN J. Biol. Chem. 259:13723-13729(1984).
RN [5]
RP SEQUENCE OF 1-2 FROM N.A.
RX MEDLINE=86313568; PubMed=3529081;
RA Nakabeppu Y., Sekiguchi M.;
RT "Regulatory mechanisms for induction of synthesis of repair enzymes
RT in response to alkylating agents: ada protein acts as a
RT transcriptional regulator.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:6297-6301(1986).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS), AND MUTAGENESIS.
RX MEDLINE=96319733; PubMed=8706135;
RA Yamagata Y., Kato M., Odawara K., Tokuno Y., Nakashima Y.,
RA Matsushima N., Yasumura K., Tomita K.-I., Ihara K., Fujii Y.,
RA Nakabeppu Y., Sekiguchi M., Fujii S.;
RT "Three-dimensional structure of a DNA repair enzyme, 3-methyladenine
RT DNA glycosylase II, from Escherichia coli.";
RL Cell 86:311-320(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
RX MEDLINE=96319734; PubMed=8706136;
RA Labahn J., Scharer O.D., Long A., Eraz-Nikpay K., Verdine G.L.,
RA Ellenberger T.E.;
RT "Structural basis for the excision repair of alkylation-damaged DNA.";
RL Cell 86:321-329(1996).
RN [8]
RP -1- FUNCTION: HYDROLYSIS OF THE DEOXYRIBOSE N-GLYCOSIDIC BOND TO
CC EXCISE 3-METHYLADENINE, 3-METHYLADENINE, 7-METHYLADENINE,
CC O2-METHYLTHIAMINE, AND O2-METHYLCTOSINE FROM THE DAMAGED DNA
CC POLYMER FORMED BY ALKYLATION LESIONS.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alkylated DNA, releasing 3-
CC methyladenine, 3-methylguanine, 7-methylguanine, and 7-
CC methyladenine.
CC -1- SUBUNIT: Monomer.
CC -1- INDUCTION: WHEN E. COLI CELLS ARE EXPOSED TO DOSES OF DNA
CC ALKYLATING AGENT. IT IS NOT INHIBITED BY REACTION PRODUCTS.
CC -1- SIMILARITY: Belongs to the alkylase DNA glycosidase alkA family.
CC -----
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CC -----
DR ENBL; K02498; AAA23430.1; -;
DR ENBL; AE000297; AAC75129.1; -;
DR ENBL; D90844; BAA15921.1; -;
DR ENBL; D90845; BAA15926.1; -;
DR ENBL; M13827; -; NOT_ANNOTATED_CDS.
DR PIR; A00904; DGECMA.
DR PDB; 1MPG; 28-JAN-98.
DR PDB; 1D12; 20-JUN-00.
DR EcoGene; EG1122; alkA.
DR InterPro; IPR000035; AlkDNA_glycosylase.
DR InterPro; IPR003265; Endo_3C.
DR Pfam; PF00710; HhH-GPD; 1.
DR SMART; SM00478; ENDO3C; 1.
DR PROSITE; PS00516; ALKYLASE_DNA_GLYCOS; 1.
KW DNA repair; Hydrolase; 3D-structure; Complete proteome.
FT SITE 218 218 DETERMINANT FOR SUBSTRATE SPECIFICITY
FT AND/OR ACTIVITY.
FT ACT_SITE 238 238 PROTON ACCEPTOR.
FT MUTAGEN 124 124 Q->A: METHYLMETHANE SULFONATE-RESISTANT.

FT MUTAGEN 218 218 W->A: NO CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-SENSITIVE.
FT MUTAGEN 237 237 D->N: MORE THAN 30% CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-RESISTANT.
FT MUTAGEN 238 238 D->N: NO CATALYTIC ACTIVITY,
FT METHYLMETHANE SULFONATE-SENSITIVE.
FT STRAND 2 5
FT HELIX 12 22
FT TURN 25 27
FT STRAND 28 30
FT STRAND 35 41
FT TURN 42 43
FT STRAND 44 53
FT TURN 54 57
FT STRAND 58 63
FT HELIX 65 70
FT HELIX 71 82
FT TURN 83 85
FT HELIX 88 95
FT HELIX 96 99
FT TURN 100 101
FT TURN 103 104
FT HELIX 113 122
FT TURN 123 125
FT HELIX 128 142
FT STRAND 145 145
FT TURN 150 151
FT STRAND 153 153
FT HELIX 158 162
FT TURN 163 163
FT HELIX 166 171
FT TURN 172 173
FT HELIX 176 191
FT TURN 192 192
FT HELIX 202 209
FT TURN 210 211
FT TURN 213 214
FT HELIX 217 227
FT TURN 236 237
FT HELIX 239 244
FT TURN 246 247
FT HELIX 250 257
FT HELIX 258 260
FT TURN 261 262
FT HELIX 264 272
FT TURN 273 273
FT TURN 275 276
SQ SEQUENCE 282 AA; 31393 MW; B66BB5E23019899C CRC64;
Query Match 80.0%; Score 32; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DMSW 5
Db 11 DMSW 14
RESULT 37
X769 HUMAN STANDARD; PRT; 295 AA.
ID X769_HUMAN
AC Q99871;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE X-linked protein STS1769.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;

```
PX MEDLINE=97254469; PubMed=9099879;
RA Esposito T., Ciccodicola A., Flagiello L., Matarazzo M.R.,
RA Migliaccio C., Cifarelli R.A., Visone R., Campanile C.,
RA Mazzarella R., Schlessinger B., D'Urso M., D'Esposito M.;
RT "Expressed STSs and transcription of human Xq28.";
RL Gene 187:185-191(1997).
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-----
CC EMBL; X99270; CRA67665.1; -.
DR Gene; HGNC:12270; TREX2.
DR InterPro; IPR003010; NCISE/CNhydase.
SQ SEQUENCE 295 AA; 33582 MW; 079BD40D8A56F45E CRC64;

Query Match 80.0%; Score 32; DB 1; Length 295;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DMSWA 6
DB 241 DWQWA 245

RESULT 38
YJGB_ECOLI
ID YJGB_ECOLI STANDARD; PRT; 339 AA.
AC P27250; P76812;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc-type alcohol dehydrogenase-like protein YjgB.
GN YjgB OR B4269.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RA Pucci M.J., Discotto L.F., Dougherty T.J.;
RA Submitted (SEP-1992) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
CC -1- COFACTOR: Binds 2 zinc ions per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
CC family.
-----
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-----
CC EMBL; M96355; AAA72122.1; -.
DR EMBL; U14003; AAA97166.1; ALT INIT.
DR EMBL; AE000497; AAC77226.1; ALT_INIT.
DR EcoGene; EGI1436; YjgB.
DR InterPro; IPR002328; ADH_zinc.

InterPro; IPR002085; Adh zn family.
DR Pfam; PF00107; Adh_zinc_N; 1.
DR PROSITE; PS00059; Adh_ZINC; 1.
KW Hypothetical protein; Oxidoreductase; Zinc; Metal-binding;
FT METAL 38 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 63 ZINC 2 (BY SIMILARITY).
FT METAL 96 ZINC 2 (BY SIMILARITY).
FT METAL 99 ZINC 2 (BY SIMILARITY).
FT METAL 102 ZINC 2 (BY SIMILARITY).
FT METAL 110 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT METAL 152 ZINC 1 (CATALYTIC) (BY SIMILARITY).
FT CONFLICT 331 YRVVKADF -> TAWC (IN REF. 1).
SQ SEQUENCE 339 AA; 36502 MW; 0854DDEFA16B9EEE CRC64;

Query Match 80.0%; Score 32; DB 1; Length 339;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSW 5
DB 130 ADWQW 134

RESULT 39
WNT2_CAEEL
ID WNT2_CAEEL STANDARD; PRT; 360 AA.
AC P34889;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Wnt-2 protein precursor.
DE Wnt-2 OR CWN-2 OR W01B6.1.
GN Wnt-2 OR CWN-2 OR W01B6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93288400; PubMed=8510930;
RA Shackelford G.M., Shivakumar S., Shiue L., Mason J., Kenyon C.,
RA Varmus H.E.;
RT "Two wnt genes in Caenorhabditis elegans.";
RL Oncogene 8:1857-1864(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Coles L.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Ligand for members of the frizzled family of seven
CC transmembrane receptors. Probable developmental protein. May be a
CC signaling molecule which affects the development of discrete
CC regions of tissues. Is likely to signal over only few cell
CC diameters.
CC -1- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -1- DEVELOPMENTAL STAGE: DETECTED IN ALL LARVAL FORMS AND ADULTS,
CC BUT IS MOST ABUNDANT IN THE EMBRYONIC STAGE.
CC -1- SIMILARITY: Belongs to the Wnt family.
-----
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-----
CC EMBL; X72943; CRA51448.1; -.
DR EMBL; Z68301; CAA92624.1; -.
DR PIR; S32695; S32695.
DR PIR; T26037; T26037.
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DR WormPep; W0186.1; CE03753.
DR InterPro; IPR005817; Wnt.
DR Pfam; PF00110; wnt; 1.
DR PRINTS; PR01349; WNTPROTEIN.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
KW wnt signaling pathway; Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 37
FT CHAIN 38 360
FT CARBOHYD 90 90
FT CONFLICT 352 352
FT CONFLICT 73 73
FT CONFLICT 186 186
FT CONFLICT 221 221
FT CONFLICT 229 230
FT CONFLICT 333 333
SQ SEQUENCE 360 AA; 40551 MW; E4A6EAF82A710F46 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 360;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 152 DWSW 155
|||||

RESULT 40
DCUP YEAST
ID _DCUP_YEAST STANDARD; PRT; 362 AA.
AC P32347;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD).
GN HEM12 OR HEM6 OR POP3 OR YD9609.03.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92249304; PubMed=1575986;
RA Garey J.R., Labbe-Bois R., Chelstowska A., Rytka J., Harrison L.,
RA Kushner J., Labbe P.;
RT "Uroporphyrinogen decarboxylase in Saccharomyces cerevisiae. HEM12
RT gene sequence and evidence for two conserved glycines essential for
RT enzymatic activity.";
RL Eur. J. Biochem. 205:1011-1016(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93348774; PubMed=8346678;
RA Diflumeri C., Larocque R., Keng T.;
RA "Molecular analysis of HEM6 (HEM12) in Saccharomyces cerevisiae, the
RT gene for uroporphyrinogen decarboxylase.";
RL Yeast 9:613-623(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Hunt S., Bowman S., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP MUTANTS.
RX MEDLINE=93111946; PubMed=1471989;
RA Chelstowska A., Zodek T., Garey J.R., Kushner J., Rytka J.,
RA Labbe-Bois R.;
RT "Identification of amino acid changes affecting yeast
RT uroporphyrinogen decarboxylase activity by sequence analysis of hem12
RT mutant alleles.";
RL Biochem. J. 288:753-757(1992).
CC CC
-1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
CO(2).
-1- PATHWAY: Porphyrin and heme biosynthesis.
-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: Belongs to the uroporphyrinogen decarboxylase family.
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-----
DR EMBL; X63721; CAA45253.1; -
DR EMBL; Z19085; CAA79514.1; -
DR EMBL; Z49209; CAA89078.1; -
DR PIR; S23471; S23471.
DR HSSP; P06132; IURO.
DR GERMOnline; 140538; -.
DR SGD; S0002454; HEM12.
DR GO; GO:0004853; F:uroporphyrinogen decarboxylase activity; IMP.
DR GO; GO:0006783; P:heme biosynthesis; IMP.
DR InterPro; IPR006361; Heme.
DR InterPro; IPR000257; Uro_decarbxs.
DR Pfam; PF01208; URO-D; 1.
DR ProDom; PD003225; Uro_decarbxs; 1.
DR TIGRfam; TIGR01464; heme; 1.
DR PROSITE; PS00906; UROD_1; 1.
DR PROSITE; PS00907; UROD_2; 1.
FT VARIANT 59 59 S -> F (IN HEM12-6 AND HEM12-12).
FT VARIANT 62 62 T -> I (IN HEM12-14).
FT VARIANT 107 107 L -> S (IN HEM12-3 AND HEM12-13).
FT VARIANT 215 215 S -> N (IN HEM12-2 AND HEM12-11).
FT MUTAGEN 33 33 G -> D: INACTIVATION.
FT MUTAGEN 300 300 G -> D: INACTIVATION.
SQ SEQUENCE 362 AA; 41349 MW; E9CB3A48E62BC277 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 362;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 280 DWSW 283
|||||

RESULT 41
HIS7_XANCP
ID HIS7_XANCP STANDARD; PRT; 375 AA.
AC P58882;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidine biosynthesis bifunctional protein hisB [Includes:
DE Histidinol-phosphatase (EC 3.1.3.15); Imidazoleglycerol-phosphate
DE dehydratase (EC 4.2.1.19) (IGPD)].
GN HISB OR XCC1811.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Camnau F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

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RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Strubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
CC -1- CATALYTIC ACTIVITY: D-erythro-1-(imidazol-4-yl)glycerol 3-
CC phosphate = 3-(imidazol-4-yl)-2-oxopropyl phosphate + H(2)O.
CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
CC + phosphate.
CC -1- PATHWAY: Histidine biosynthesis; sixth step.
CC -1- PATHWAY: Histidine biosynthesis; eighth step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: In the N-terminal section; belongs to the histidinol-
CC phosphatase family.
CC -1- SIMILARITY: In the C-terminal section; belongs to the
CC imidazoleglycerol-phosphate dehydratase family.
CC -----
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CC -----
DR EMAP; AE012283; AAM41100.1; -.
DR HAMAP; MF 01022; -.
DR InterPro; IPR006549; HAD-SP-III.A.
DR InterPro; IPR005954; HisB_N.
DR InterPro; IPR006543; Histidinol-phos.
DR InterPro; IPR000807; IGPD.
DR Pfam; PF00475; IGPD; 1.
DR ProDom; PD002282; IGPD; 1.
DR TIGRFAMs; TIGR01662; HAD-SP-III.A; 1.
DR TIGRFAMs; TIGR01261; HisB_Nterm; 1.
DR TIGRFAMs; TIGR01656; Histidinol-ppas; 1.
DR PROSITE; PS00954; IGP_DEHYDRATASE_1; 1.
DR PROSITE; PS00955; IGP_DEHYDRATASE_2; 1.
DR Histidine biosynthesis; Multifunctional enzyme; Lyase; Hydrolase;
KW Complete proteome.
KW DOMAIN 1 168 HISTIDINOL-PHOSPHATASE.
FT DOMAIN 159 375 IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE.
FT SEQUENCE 375 AA; 41812 MW; 758A9F43F0FAF72 CRC64;
SQ
Query Match 80.0%; Score 32; DB 1; Length 375;
Best Local Similarity 100.0%; Pred. NO. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 DSWA 6
DB 154 DWDWA 158
RESULT 42
FOLC_BUCAI
ID FOLC_BUCAI STANDARD; PRT; 411 AA.
AC P57265;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE FOLC bifunctional protein [includes: Folylpolyglutamate synthase
DE (EC 6.3.2.17) (Folylpoly-gamma-glutamate synthetase) (FPGS);
DE Dihydrofolate synthase (EC 6.3.2.12)].
GN FOLC OR BU167.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
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OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RC MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -1- FUNCTION: Conversion of folates to polyglutamate derivatives.
CC -1- CATALYTIC ACTIVITY: ATP + {tetrahydrofolyl-(Glu)}(N) + L-glutamate
CC = ADP + phosphate + {tetrahydrofolyl-(Glu)}(N+1).
CC -1- CATALYTIC ACTIVITY: ATP + dihydropterate + L-glutamate = ADP +
CC phosphate + dihydrofolate.
CC -1- PATHWAY: Folate biosynthesis.
CC -1- SIMILARITY: Belongs to the folylpolyglutamate synthase family.
CC -----
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CC -----
DR EMBL; AF001118; BAB12885.1; -.
DR HSSP; P15925; 1FGS.
DR InterPro; IPR001645; Fpolygl_synthase.
DR InterPro; IPR000713; Mur_ligase.
DR Pfam; PF01225; Mur_ligase; 1.
DR TIGRFAMs; TIGR01499; folC; 1.
DR PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; 1.
DR PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; FALSE_NEG.
KW Multifunctional enzyme; Ligase; One-carbon metabolism; ATP-binding;
KW Folate biosynthesis; Complete proteome.
FT NP BIND 50 56 ATP (BY SIMILARITY).
SQ SEQUENCE 411 AA; 46970 MW; 5DDC2DC6539935A CRC64;
Query Match 80.0%; Score 32; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DWSW 5
DB 220 DWSW 223
RESULT 43
HLT_VIBPA
ID HLT_VIBPA STANDARD; PRT; 418 AA.
AC Q99289;
DT 01-FEB-1995 (Rel. 31, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thermolabile hemolysin precursor (TL) (lecithin-dependent haemolysin)
DE (LDH) (Atypical phospholipase) (Phospholipase A2) (Lysophospholipase).
GN VPA0226.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=89237825; PubMed=3508495;
RA Taniguchi H., Hirano H., Kubomura S., Higashi K., Mizuguchi Y.;
RT "Comparison of the nucleotide sequences of the genes for the
RT thermostable direct hemolysin and the thermolabile hemolysin from
RT Vibrio parahaemolyticus.";
RL Microb. Pathog. 1:425-432(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RC MEDLINE=22508454; PubMed=12620739;
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RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of *Vibrio parahaemolyticus*: a pathogenic mechanism
RL distinct from that of *V. cholerae*.";
RL Lancet 361:743-749 (2003).
RN [3]
RP SEQUENCE OF 20-47, AND CHARACTERIZATION.
RX MEDLINE=92166705; PubMed=1791426;
RA Shinoda S., Matsuoka H., Tsuchie T., Miyoshi S.-I., Yamamoto S.,
RA Taniguchi H., Mizuguchi Y.;
RT "Purification and characterization of a lecithin-dependent haemolysin
RT from *Escherichia coli* transformed by a *Vibrio parahaemolyticus*
RT gene.";
RL J. Gen. Microbiol. 137:2705-2711 (1991).
CC -1- FUNCTION: Phospholipase hydrolyzing both fatty acid esters of
CC phospholipid, i.e., it hydrolyzes phosphatidylcholine (PC) to
CC lysophosphatidylcholine (LPC) and then LPC to
CC glycerophosphorylcholine (GPC).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PFM: There are two forms of LDH. The LDH(S) may be a protein in
CC which 13 residues of the N-terminal of LDH(L) are deleted.
CC -1- SIMILARITY: Belongs to the "GDSL" family of lipolytic enzymes.
CC
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CC
CC EMBL; M36437; AAA27526.1; -;
CC EMBL; AP005084; BAC61569.1; -;
CC PIR; A53888; A53888.
CC InterPro; IPR001087; Lipase GDSL.
CC InterPro; IPR008265; Lipase_GDSL_AS.
CC Pfam; PF00657; Lipase_GDSL; 1.
CC PROSITE; PS01098; LIPASE_GDSL_SER; 1.
CC Hydrolyase; Lipid degradation; Hemolysis; Toxin; Signal;
CC Complete proteome.
FT SIGNAL 1 19
FT CHAIN 20 418 THERMOLABILE HEMOLYSIN.
FT ACT_SITE 153 153 BY SIMILARITY.
FT ACT_SITE 395 395 POTENTIAL.
FT VARIANT 20 32 MISSING (IN LDH(S)).
FT CONFLICT 20 20 A -> T (IN REF. 3).
FT CONFLICT 219 219 E -> D (IN REF. 1).
FT CONFLICT 390 390 D -> N (IN REF. 1).
SQ SEQUENCE 418 AA; 47392 MW; DC59A641DD04B1BD CRC64;

Query Match 80.0%; Score 32; DB 1; Length 418;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 63 DWEWA 67

RESULT 44
NRAM IAWIL STANDARD; PRT; 453 AA.
AC P03470;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Wilson-Smith/33).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11487;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82192605; PubMed=7077751;
RA Hiti A.L., Nayak D.P.;
RT "Complete nucleotide sequence of the neuraminidase gene of human
RL influenza virus A/WSN/33.";
RL J. Virol. 41:730-734 (1982).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
CC EMBL; J02177; AAA43397.1; ALT_SEQ.
CC HSP; P03472; QWC.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00084; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 35 ANCHOR.
FT DOMAIN 36 74 HYPervARIABLE STALK REGION.
FT DOMAIN 75 453 HEAD OF NEURAMINIDASE.
FT ACT_SITE 259 259 PROBABLE.
FT ACT_SITE 261 261 PROBABLE.
FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 453 AA; 49623 MW; 7DC56A4416A47BE8 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 438 DWSW 441

RESULT 45
NRAM IAPUE STANDARD; PRT; 454 AA.
AC P03468;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Puerto Rico/8/34).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11455;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81148841; PubMed=7010182;
RA Fields S., Winter G., Brownlee G.G.;
RT "Structure of the neuraminidase gene in human influenza virus
RT A/PR/8/34.";

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RL Nature 290:213-217(1981).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC
CC EMBL: J02146; AAA43412.1; -.
CC HSP: P03472; 20WC.
CC InterPro: IPR001860; Glyco_hydro_34.
CC Pfam: PF00064; neu; 1.
CC ProDom: PD000431; Glyco_hydro_34; 1.
CC Hydrolase: Glycosidase; Glycoprotein; Transmembrane.
CC TRANSMEM 7 ANCHOR.
CC DOMAIN 36 75 HYPERVARIABLE STALK REGION.
CC FT DOMAIN 76 454 HEAD OF NEURAMINIDASE.
CC FT ACT SITE 260 260 PROBABLE.
CC FT ACT SITE 262 262 PROBABLE.
CC FT CARBOHYD 44 44 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 58 58 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 131 131 N-LINKED (GLCNAC. .) (POTENTIAL).
CC FT CARBOHYD 220 220 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 454 AA; 50143 MW; A0DC4C08A2B53705 CRC64;
SQ
Query Match 80.0%; Score 32; DB 1; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DMSW 5
DB 439 DWSW 442
PRT; 470 AA.
RESULT 46
NOS2_ONCMY STANDARD; PRT; 470 AA.
AC Q92091;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Nitric oxide synthase, inducible [EC 1.14.13.39] (NOS, type II)
DE (Inducible NOS) (INOS) (Fragment).
GN NOS2.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RA Grabowski P.S., Laing K.J., Hardie L., Macguigan F., Ralston S.,
RA Secombes C.J.;
RT "Detection of mRNA for a nitric oxide synthase in macrophages and
RT gill of rainbow trout challenged with an attenuated bacterial
RT pathogen."
RL (in) Moncada S., Stamler J., Gross S., Higgs E.A. (eds.);
RL 4th International meeting on the biology of nitric oxide, Amelia

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RL Island, Florida, Sep. 1995, pp.10:48-48, Portland Press,
RL Brookfield (1996).
CC -1- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule
CC with diverse functions throughout the body. In macrophages, NO
CC mediates tumoricidal and bactericidal actions.
CC -1- CATALYTIC ACTIVITY: L-arginine + NADPH + H+ = citrulline +
CC nitric oxide + NADP(+).
CC -1- COFACTOR: Heme. Binds one mole each of FAD and FMN. Also requires
CC tetrahydrobiopterin (BH4) which may stabilize the dimeric form of
CC the enzyme (By similarity).
CC -1- ENZYME REGULATION: Not stimulated by calcium/calmodulin (By
CC similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SIMILARITY: Belongs to the NOS family.
CC -1- SIMILARITY: Contains 1 flavodoxin-like domain.
CC
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CC
CC EMBL: X97013; CAA65736.1; -.
CC HSP: P29477; INOS.
CC InterPro: IPR003097; FAD binding.
CC InterPro: IPR008254; Flavodoxin_Like.
CC InterPro: IPR001094; Flavodoxin_Like.
CC InterPro: IPR004030; NO synthase.
CC Pfam: PF00667; FAD_binding_1; 1.
CC Pfam: PF02898; NO synthase; 1.
CC PRINTS: PR00369; FLAVODOXIN.
CC PROSITE: PS0902; FLAVODOXIN LIKE; 1.
CC PROSITE: PS60001; NOS; PARTIAL.
CC OXidoreductase; NADP; FAD; FMN; Calmodulin-binding; Heme.
FT NON_TER 1
FT DOMAIN 139 159 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 169 307 FLAVODOXIN-LIKE.
FT NP_BIND 253 284 FMN (PYRIMIDINE PART) (BY SIMILARITY).
FT NP_BIND 398 409 FAD (ADP PART) (BY SIMILARITY).
FT NON_TER 470 470
SQ SEQUENCE 470 AA; 53329 MW; 40B6717EE500B64D CRC64;
Query Match 80.0%; Score 32; DB 1; Length 470;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ADKSW 5
DB 89 ADKDW 93
PRT; 483 AA.
RESULT 47
ENGA_BRUME STANDARD; PRT; 483 AA.
AC Q8YF42;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE GTP-binding protein engA.
GN ENGA OR BWE11550.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=16M / ATCC 23456 / Biotype 1;
RX MEDLINE=20020109; PubMed=11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujar C., Los T.,
RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

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RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltzman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Lelesson J.-J.,
RA Haeckl Korn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
RT *Brucella melitensis*.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
CC -1- FUNCTION: GTPase of unknown physiological role.
CC -1- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. EngA subfamily.
CC -----
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CC -----
CC EMBL; AE009590; AAL52731.1; -;
CC PIR; AH3445; AH3445.
CC HAMAP; MF 00195; -; 1.
CC InterPro; IPR005289; GTP-binding_dom.
CC InterPro; IPR006073; GTP1_OBG.
CC InterPro; IPR002917; MMR_HSR1.
CC InterPro; IPR001806; Ras_trnsfrmg.
CC Pfam; PF01926; MMR_HSR1; 1.
CC PRINTS; PR00449; RASTNSFRMNG.
CC TIGRFAMs; TIGR00650; MG442; 2.
CC TIGRFAMs; TIGR00231; small_GTP; 2.
CC GTP-binding; Repeat; Complete proteome.
CC NP_BIND 9 16 GTP 1 (POTENTIAL).
CC FT NP_BIND 56 60 GTP 1 (POTENTIAL).
CC FT NP_BIND 119 122 GTP 1 (POTENTIAL).
CC FT NP_BIND 218 225 GTP 2 (POTENTIAL).
CC FT NP_BIND 265 269 GTP 2 (POTENTIAL).
CC FT NP_BIND 330 333 GTP 2 (POTENTIAL).
CC SQ SEQUENCE 483 AA; 53311 MW; 16241111DB29AA266 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 483;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 252 ADMEW 256

RESULT 48
ID ENGA BRUSU STANDARD; PRT; 483 AA.
AC OBG2E8;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE GTP-binding protein engA.
GN ENGA OR BR0375.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Sebahdri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Unayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kral M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tetzelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The *Brucella suis* genome reveals fundamental similarities between

RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
CC -1- FUNCTION: GTPase of unknown physiological role.
CC -1- SIMILARITY: Belongs to the era/trmE family of GTP-binding
CC proteins. EngA subfamily.
CC -----
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CC -----
CC EMBL; AE014349; AAN29321.1; -;
CC TIGR; BR0375; -;
CC HAMAP; MF 00195; -; 1.
CC InterPro; IPR005289; GTP-binding_dom.
CC InterPro; IPR006073; GTP1_OBG.
CC InterPro; IPR002917; MMR_HSR1.
CC InterPro; IPR001806; Ras_trnsfrmg.
CC Pfam; PF01926; MMR_HSR1; 1.
CC PRINTS; PR00326; MMR_HSR1; 1.
CC PRINTS; PR00449; RASTNSFRMNG.
CC TIGRFAMs; TIGR00650; MG442; 2.
CC TIGRFAMs; TIGR00231; small_GTP; 2.
CC GTP-binding; Repeat; Complete proteome.
CC NP_BIND 9 16 GTP 1 (POTENTIAL).
CC FT NP_BIND 56 60 GTP 1 (POTENTIAL).
CC FT NP_BIND 119 122 GTP 1 (POTENTIAL).
CC FT NP_BIND 218 225 GTP 2 (POTENTIAL).
CC FT NP_BIND 265 269 GTP 2 (POTENTIAL).
CC FT NP_BIND 330 333 GTP 2 (POTENTIAL).
CC SQ SEQUENCE 483 AA; 53281 MW; 776B950CFA036EF3 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 483;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 252 ADMEW 256

RESULT 49
ID YC42 SYN3 STANDARD; PRT; 536 AA.
AC P423T9;
DT 01-NOV-1995 (Rel. 32, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical methyltransferase all1242 (EC 2.1.1.-) (ORF N).
GN SL1242.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugikura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT *Synechocystis* sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
RN [2]
RP SEQUENCE OF 291-536 FROM N.A.
RX MEDLINE=93222488; PubMed=8467083;
RA Malakhov M.P., Wada H., Los D.A., Sakamoto T., Murata N.;

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RT "Structure of a cyanobacterial gene encoding the 50S ribosomal protein L9.";
RL Plant Mol. Biol. 21:913-918(1993).
CC -1- SIMILARITY: TO METHYLTRANSFERASES.

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CC EMBL; D90912; BAA18175.1; -;
DR EMBL; D10716; BAA38817.1; -;
DR PIR; S75614; S75614.
DR InterPro; IPR006158; B12-binding.
DR InterPro; IPR006638; Elp3.
DR InterPro; IPR007197; Radical SAM.
DR Pfam; PF02310; B12-binding; 1.
DR Pfam; PF04055; Radical SAM; 1.
DR SMART; SM00729; Elp3; 1.
DR Hypothetical protein; Transferase; Methyltransferase;
KW Complete proteome.
SQ SEQUENCE 536 AA; 61755 MW; 715F06F2C2D684E3 CRC64;

Query Match 80.0%; Score 32; DB 1; Length 536;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6
| : | | |
DB 61 AEWDWA 66

RESULT 50

DNJM MYCGE STANDARD; PRT; 601 AA.
ID DNJM MYCGE STANDARD; PRT; 601 AA.
AC P47442; Q49288;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DnaJ-like protein MG200.
GN MG200.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Karlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium";
RL Science 270:397-403(1995).
RN [2]
RN SEQUENCE OF 281-409 FROM N.A.
RP STRAIN=ATCC 33530 / G-37;
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
CC -1- SIMILARITY: Contains 1 J domain.

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Query Match 80.0%; Score 32; DB 1; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
| : | | |
DB 186 DWSW 189

Search completed: July 23, 2004, 13:18:40
Job time : 15 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:14:39 ; Search time 35 Seconds
(without alignments)
54.089 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	37	92.5	236 3 Q8NJY9	Q8NJY9 bionectria
2	37	92.5	274 16 Q8G659	Q8G659 bifidobacte
3	37	92.5	375 5 Q86K30	Q86K30 dictyosteli
4	37	92.5	437 16 Q92K30	Q92K30 rhizobium m
5	37	92.5	548 16 Q92M15	Q92M15 rhizobium m
6	37	92.5	581 5 Q8MSH3	Q8MSH3 drosophila
7	37	92.5	597 5 Q9VGP2	Q9VGP2 drosophila
8	37	92.5	610 16 Q86712	Q86712 streptomyce
9	37	92.5	885 16 Q9I389	Q9I389 pseudomonas
10	36	90.0	173 16 Q82SE1	Q82SE1 streptomyce
11	36	90.0	205 16 Q9ACR5	Q9ACR5 streptomyce
12	36	90.0	227 4 Q8IXK8	Q8IXK8 homo sapien
13	36	90.0	228 8 Q7YUG8	Q7YUG8 sphenodon p
14	36	90.0	242 12 Q919K8	Q919K8 culcx nigri
15	36	90.0	355 11 Q8BIT9	Q8BIT9 mus musculu
16	36	90.0	358 10 Q50002	Q50002 prunus arme

17	36	90.0	374	16	Q9HZ10	Q9HZ10 pseudomonas
18	36	90.0	426	5	Q86KF9	Q86KF9 dictyosteli
19	36	90.0	433	16	Q8P4A1	Q8P4A1 xanthomonas
20	36	90.0	438	16	Q8PFV8	Q8PFV8 xanthomonas
21	36	90.0	452	4	Q96AB7	Q96AB7 homo sapien
22	36	90.0	463	5	Q8MMJ0	Q8MMJ0 apis cerana
23	36	90.0	470	12	Q7TF27	Q7TF27 influenza a
24	36	90.0	477	11	Q9CYU6	Q9CYU6 mus musculu
25	36	90.0	484	4	Q9BTU6	Q9BTU6 homo sapien
26	36	90.0	605	16	Q82MX2	Q82MX2 streptomyce
27	36	90.0	686	16	Q8FQZ9	Q8FQZ9 corynebacte
28	36	90.0	861	16	Q88NQ1	Q88NQ1 pseudomonas
29	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
30	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arabidopsis
31	36	90.0	1324	16	Q820F9	Q820F9 streptomyce
32	36	90.0	5435	2	Q9L4X2	Q9L4X2 streptomyce
33	35	87.5	527	16	Q829Q9	Q829Q9 streptomyce
34	34	85.0	166	4	Q8NBW1	Q8NBW1 homo sapien
35	34	85.0	273	10	Q94JM4	Q94JM4 arabidopsis
36	34	85.0	273	10	Q940D6	Q940D6 arabidopsis
37	34	85.0	275	10	Q65710	Q65710 arabidopsis
38	34	85.0	337	11	Q80UX8	Q80UX8 mus musculu
39	34	85.0	376	3	Q9UVL4	Q9UVL4 penicillium
40	34	85.0	617	10	P930S0	P930S0 arabidopsis
41	34	85.0	1074	16	Q8E170	Q8E170 xanthomonas
42	34	85.0	1842	3	Q96WT6	Q96WT6 schizosacch
43	34	85.0	1842	3	Q96WT7	Q96WT7 schizosacch
44	34	85.0	1842	3	Q96WT8	Q96WT8 schizosacch
45	33	82.5	49	6	Q8SPL6	Q8SPL6 equus cabal
46	33	82.5	98	5	Q9VB45	Q9VB45 drosophila
47	33	82.5	136	2	Q8KZ39	Q8KZ39 uncultured
48	33	82.5	154	11	Q8BGD2	Q8BGD2 mus musculu
49	33	82.5	155	16	Q82IK8	Q82IK8 chlamydomophi
50	33	82.5	159	10	Q84UN9	Q84UN9 oryza sativ

ALIGNMENTS

RESULT 1

Q8NJY9	Q8NJY9	PRELIMINARY;	PRT;	236 AA.
AC	Q8NJY9;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Endoglucanase.			
GN	CEL12C.			
OS	Bionectria ochroleuca (Gliocladium roseum).			
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;			
OC	Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.			
OX	NCBI_TaxID=29856;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-22067395; PubMed-12073090;			
RA	Goedegebuur F., Fowler T., Phillips J., van der Kley P.,			
RA	van Solingen P., Dankmeyer L., Power S.D.;			
RT	"Cloning and relational analysis of 15 novel fungal endoglucanases			
RT	from family 12 glycosyl hydrolase.";			
RL	Curr. Genet. 41:89-98(2002).			
DR	EMBL, AF435065; AM77708.1;			
DR	GO; GO:000810; P:cellulase activity; IEA.			
DR	GO; GO:0000272; P:polysaccharide catabolism; IEA.			
DR	InterPro; IPR008985; ConA like lec.gl.			
DR	InterPro; IPR002594; Glyco_hydro_12.			
DR	Pfam; PF01670; Glyco_hydro_12; 1_			
DR	ProDom; PD004316; Glyco_hydro_12; 1_			
SQ	SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;			
Query Match 92.5%; Score 37; DB 3; Length 236;				
Best Local Similarity 83.3%; Pred. No. 2.3e+02;				
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;				

QY 1 ADWSWA 6
Db 63 ADWSWS 68

RESULT 2

Q8G659 Q8G659 PRELIMINARY; PRT; 274 AA.

AC Q8G659; 01-MAR-2003 (TREMBlrel. 23, Created)

DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Probable dihydroxotrate dehydrogenase electron transfer subunit.

GN PYRK OR BL0790.

OS Bifidobacterium longum.

OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;

OC Bifidobacteriaceae; Bifidobacterium.

OX NCBI_TaxID=216816;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCC 2705;

RX MEDLINE=22294977; PubMed=12381787;

RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,

RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,

RA Primrose R.D., Argison F.,

RA "The genome sequence of Bifidobacterium longum reflects its adaptation

RT to the human gastrointestinal tract.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427 (2002).

DR EMBL; AE014701; AAN24605.1; -.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0006118; P:electron transport; IEA.

DR InterPro; IPR008333; PAD_binding_6.

DR Pfam; PF00970; PAD_binding_6; 1.

KW Complete proteome.

SQ SEQUENCE 274 AA; 29978 MW; 97180016E79636DB CRC64;

Query Match 92.5%; Score 37; DB 16; Length 274;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
Db 171 ADWSWS 176

RESULT 3

Q86KS0 Q86KS0 PRELIMINARY; PRT; 375 AA.

AC Q86KS0; 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Hypothetical protein.

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

OX NCBI_TaxID=44689;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=AX4;

RX MEDLINE=22092622; PubMed=12097910;

RA Glockner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,

RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,

RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.,

RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";

RL Nature 418:79-85 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=AX4;

RA Baugart C.;

RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC115612; AAO50929.1; -.

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puhler A., Purnelle B., Rampsberger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.,
RT "Analysis of the chromosome sequence of the legume symbiont
RL Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL; AL591791; CAC47210.1; -;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005244; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00211; ABC TRANSPORTER 1; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;
Query Match 92.5%; Score 37; DB 16; Length 548;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 235 ADMAWA 240
|||||
RESULT 6
Q8MSH3 ID Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GH24640p.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fiesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houson K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lammel P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.-Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003691; AAP54634.1; -;
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred.C.
DR InterPro; IPR00169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred C; 1.
DR Pfam; PF00732; GMC_oxred N; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
Qy 1 ADWSWA 6
Db 235 ADMAWA 240
|||||
Query Match 92.5%; Score 37; DB 5; Length 581;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6

Db 158 SDMSWA 163
|||||
RESULT 7
Q9VGP2 ID Q9VGP2 PRELIMINARY; PRT; 597 AA.
AC Q9VGP2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG6728 protein.
GN NINAG OR CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Hostin D., Houson K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S.-Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003691; AAP54634.1; -;
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred.C.
DR InterPro; IPR00169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred C; 1.
DR Pfam; PF00732; GMC_oxred N; 1.
DR PROSITE; PS00624; GMC_OXRED_2; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

Mon Jul 26 09:11:31 2004

SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFA902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;
 Best Local Similarity 83.3%; Pred. No. 5.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 :|||||
 Db 158 SDWSWA 163

RESULT 8

ID O86712 PRELIMINARY; PRT; 610 AA.

AC O86712; (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Hypothetical protein SC06530.

GN SC06530 OR SC5C7.15.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2) / M145;

RX MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Carris D.E., Quail M.A., Kieser H.,
 Thomson N.R., James K.D., Hendon S., Chandra G., Chen C.W., Collins M.,
 Harper D., Bateman A., Brown S., Hidalgo J., Hornsby T., Howarth S.,
 Cronin A., Fraser A., Goble A., Hildalgo J., Murphy L., Oliver K., O'Neil S.,
 Huang C.-H., Kieser T., Larke L., Murphree L., Oliver K., O'Neil S.,
 Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 Hopwood D.A.

RA "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";

RL Nature 417:141-147(2002).

DR EMBL; AL939128; CAA20627.1; --

DR PIR; T35222; T35222.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 610;
 Best Local Similarity 83.3%; Pred. No. 5.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 :|||||
 Db 83 ADWSWA 88

RESULT 9

ID Q91389 PRELIMINARY; PRT; 885 AA.

AC Q91389; (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Two-component sensor KdpD.

GN KDPD OR PA1636.

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 15692 / PAO1;

RX MEDLINE=20437337; PubMed=10984043;

RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
 opportunistic pathogen.";
 Nature 406:959-964(2000).

RL -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.

CC EMBL; AE004591; AAG05025.1; --

DR FIR; C83441; C83441.

DR HSP; P02933; IJOY.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.

DR GO; GO:0006950; P:response to stress; IEA.

DR GO; GO:0007600; P:sensory perception; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR003594; ATPbind_ATPase.

DR InterPro; IPR004358; Bact_sens_pr_C.

DR InterPro; IPR003018; GAF.

DR InterPro; IPR005467; His_kinase.

DR InterPro; IPR003661; His_kinA_N.

DR InterPro; IPR003852; KdpD.

DR InterPro; IPR006016; Usp_dom.

DR Pfam; PF02518; HATPase_C; 1.

DR Pfam; PF02702; KdpD; 1.

DR Pfam; PF02512; HisKA; 1.

DR Pfam; PF02702; KdpD; 1.

DR PRINIS; PR003444; BCTRLSENSOR.

DR PRODOM; PD011725; KdpD; 1.

DR SMART; SM00065; GAF; 1.

DR SMART; SM00387; HATPase_C; 1.

DR SMART; SM00388; HisKA; 1.

DR PROSITE; P550109; HIS_KIN; 1.

KW Kinase; Phosphorylation; Sensory transduction; Transferase;

KW Complete Proteome.

SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;
 Best Local Similarity 83.3%; Pred. No. 8.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 :|||||
 Db 563 ADWSWA 568

RESULT 10

Q825E1 PRELIMINARY; PRT; 173 AA.

ID Q825E1

AC Q825E1; (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Hypothetical protein.

GN SAV7517.

OS Streptomyces avermitilis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=33903;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

RX MEDLINE=21477403; PubMed=11572948;

RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
 Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
 "Genome sequence of an industrial microorganism Streptomyces
 avermitilis: deducing the ability of producing secondary
 metabolites.";
 Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

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[2]
RN SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005050; BAC75228.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 173 AA; 18912 MW; 22826C7D2222CA60 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 173;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 53 ADWEWA 58

RESULT 11
Q9ACR5 PRELIMINARY; PRT; 205 AA.
ID Q9ACR5;
AC Q9ACR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCF1.253.
GN SCF1.253.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Horsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36779.1; -
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93FD9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 10 ADWSW 14

RESULT 12
Q8IXK8 PRELIMINARY; PRT; 227 AA.
ID Q8IXK8;
AC Q8IXK8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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DE Similar to hypothetical protein BC017335.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC040173; AAH40173.1; -
KW Hypothetical protein.
SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 113 ADWSW 117

RESULT 13
Q7YGU8 PRELIMINARY; PRT; 228 AA.
ID Q7YGU8;
AC Q7YGU8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome oxidase subunit II.
OS Sphenodon punctatus (Hatteria) (Tuatara).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
OX NCBI_TaxID=8508;
RN [1]
RP SEQUENCE FROM N.A.
RA Rest J.S., Ast J.C., Austin C.C., Maddell P.J., Tibbetts E.A.,
RA Hay J.M., Mindell D.P.;
RT "Molecular systematics of primary reptilian lineages and the tuatara
RT mitochondrial genome.";
RL Mol. Phylogenet. Evol. 0:0-0(2003).
DR EMBL; AF534390; AAP42708.1; -
KW Mitochondrion.
SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;

Query Match 90.0%; Score 36; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 221 DWSWA 225

RESULT 14
Q919K8 PRELIMINARY; PRT; 242 AA.
ID Q919K8;
AC Q919K8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CUN068 hypothetical protein.
GN CUN068.
OS Culex nigripalpus baculovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
OX NCBI_TaxID=130556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RX MEDLINE=21488685; PubMed=11602755;
RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,

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RA Becnel J.J., Rock D.L., Kutish G.F.;
RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
RN J. Virol. 75:11157-11165(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Florida1997;
RA Afonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
RA Becnel J.J., Rock D.L., Kutish G.F.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF403738; AAK94146.1; -;
KW Hypothetical protein.
SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 80 DWSWA 84
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RESULT 15
Q8BIT9 PRELIMINARY; PRT; 355 AA.
AC Q8BIT9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitochondrial ribosomal protein L41 homolog.
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK087998; BAC40084.1; -;
DR MGD; MGI:1914478; 2810443J12RIK.
DR InterPro; IPR001580; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD REPEATS_1; 1.
DR PROSITE; PS50294; WD REPEATS_REGION; 1.
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match 90.0%; Score 36; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 215 ADMSW 219
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RESULT 16
OS0002 PRELIMINARY; PRT; 358 AA.
AC OS0002;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;
RA Mdeguile-A-Mdeguile D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of AFPL1, a Cysteine Proteinase From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179).";
RL Plant Physiol. 115:1730-1730(1997).
RW EMBL; U93166; AAB97142.1; -;
KW HSSP; P07711; ICJL.
DR MEROPS; C01.041; -;
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CIS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 108 ADMSW 112
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|||||

RESULT 17
Q9HZ10 PRELIMINARY; PRT; 374 AA.
AC Q9HZ10;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RW EMBL; AE004746; AAG06618.1; -;
DR PIR; B83241; B83241.
DR InterPro; IPR007434; DUF482.
DR Pfam; PF04339; DUF482; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;


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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 81 DWSWA 85

RESULT 18
Q86KF9 PRELIMINARY; PRT; 426 AA.
AC Q86KF9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to Mus musculus (Mouse). DnaJ homolog subfamily B member 5
DE (Heat shock protein Hsp40-3) (Heat shock protein cognate 40)
DE (Hsc40).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostellium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Farra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RA "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RA Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AC115680; AA051091.1; -.
DR GO; GO:0003773; P:heat shock protein activity; IEA.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR003095; Hsp_DnaJ.
DR Pfam; PF00226; DnaJ; 1.
DR PRINTS; PR06625; DNAJPROTEIN.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
KW Heat shock.
SQ SEQUENCE 426 AA; 48376 MW; EBF9F3729595727 CRC64;

Query Match 90.0%; Score 36; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 127 DWSWA 131

RESULT 19
Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.0%; Score 36; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 127 DWSWA 131

RESULT 19
Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.0%; Score 36; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 181 DWSWA 185

RESULT 20
Q8PFV8 PRELIMINARY; PRT; 438 AA.
AC Q8PFV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Matsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012502; AAM43483.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease region.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EF217D2A7C516533 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 181 DWSWA 185

RESULT 20
Q8PFV8 PRELIMINARY; PRT; 438 AA.
AC Q8PFV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Matsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE012036; AAM38706.1; -.

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 183 DWSWA 187

RESULT 21
ID Q96AB7 PRELIMINARY; PRT; 452 AA.
AC Q96AB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AAH17335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25E838096733 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 338 ADWSW 342

RESULT 22
ID Q8MMJ0 PRELIMINARY; PRT; 463 AA.
AC Q8MMJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permeasel.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 183 DWSWA 187

RESULT 21
ID Q96AB7 PRELIMINARY; PRT; 452 AA.
AC Q96AB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017335; AAH17335.1; -.
DR EMBL; AK075115; BAC11411.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS00082; WD_REPEATS_2; 1.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25E838096733 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 338 ADWSW 342

RESULT 22
ID Q8MMJ0 PRELIMINARY; PRT; 463 AA.
AC Q8MMJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.
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GN MRJP2.
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7461;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nurse heads;
RA Sittipraneed S., Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525777; AAM88282.1; -.
DR InterPro; IPR003534; Royaljelly.
DR Pfam; PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;

Query Match 90.0%; Score 36; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 110 DWSWA 114

RESULT 23
Q7TF27
ID Q7TF27 PRELIMINARY; PRT; 470 AA.
AC Q7TF27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuraminidase.
OS Influenza A virus (A/duck/NY/191255-59/02 (H5N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=232442;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/duck/NY/191255-59/02;
RA Lee C.-W., Senne D., Linares J.A., Woolcock P., Stallnecht D.,
RA Spackman E., Swayne D., Suarez D.;
RT "Characterization of recent H5 subtype avian influenza viruses from
RT U.S. poultry.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY300948; AAP57560.1; -.
SQ SEQUENCE 470 AA; 52260 MW; 41470434D8ED1662 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 470;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 453 ADWSW 457

RESULT 24
Q9CYU6
ID Q9CYU6 PRELIMINARY; PRT; 477 AA.
AC Q9CYU6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2810443J12Rik protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12RIK.
OS Mus musculus (Mouse).
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa K., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Aehburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staebli F., Suzuki K., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Mesonephros;
 RX MEDLINE=22354683; PubMed=12468851;
 RA The FANTOM Consortium,
 RA "The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK013297; BAB28775.1; -;
 DR EMBL; AK078448; BAC37279.1; -;
 DR MGD; MGI:1914478; 2810443J12Rik.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 4.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 1.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 SQ SEQUENCE 477 AA; 53201 MW; 26555735244A9C CRC64;
 Query Match 90.0%; Score 36; DB 11; Length 477;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 DB 337 ADMSW 341
 ID Q9BTV6 PRELIMINARY; PRT; 484 AA.
 AC Q9BTV6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC003123; AAH03123.1; -;
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS50082; WD_REPEATS_2; 1.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Hypothetical protein; Repeat; WD repeat.
 FT NON TER 1
 SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7359E CRC64;
 Query Match 90.0%; Score 36; DB 4; Length 484;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 DB 370 ADMSW 374
 ID Q82MX2 PRELIMINARY; PRT; 605 AA.
 AC Q82MX2;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Putative nitric oxide synthase.
 GN SAV1531.
 OS Streptomyces avermitilis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=33903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=21477403; PubMed=11572948;
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
 RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,
 RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
 RT "Genome sequence of an industrial microorganism Streptomyces
 RT avermitilis: deducing the ability of producing secondary
 RT metabolites.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 RX MEDLINE=22608306; PubMed=12692562;
 RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
 RA Sakaki Y., Hattori M., Omura S.,
 RT "Complete genome sequence and comparative analysis of the industrial
 RT microorganism Streptomyces avermitilis.";
 RL Nat. Biotechnol. 21:526-531(2003).
 DR EMBL; AP005027; BAC69241.1; -;
 DR GO; GO:0004517; F: Nitric-oxide synthase activity; IEA.
 DR GO; GO:0006809; P: Nitric oxide biosynthesis; IEA.
 DR InterPro; IPR004030; NO synthase.
 DR Pfam; PF02898; NO synthase; 1.
 DR PROSITE; PS60001; NOS; 1.
 KW Complete proteome.
 SQ SEQUENCE 605 AA; 65534 MW; 8208F93B381C1FF5 CRC64;
 Query Match 90.0%; Score 36; DB 16; Length 605;
 Best Local Similarity 100.0%; Pred. No. 8.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 DB 556 ADMSW 560
 ID Q9BTV6 PRELIMINARY; PRT; 484 AA.
 AC Q9BTV6;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;

RESULT 27

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Q8FQ29      Q8FQ29      PRELIMINARY;      PRT;      686 AA.
AC
Q8FQ29;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative ATP-dependent DNA helicase.
GN CE0968.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Kawabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,
RA Ikeo K., Sugimoto M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,
RA Usuda Y., Sugimoto S.;
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005217; BAC17778.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP dependent helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0006259; P:DNA metabolism; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR002464; DEAH_box.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR004589; RecQ.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR TIGRFAMs; TIGR00614; recQ_fam; 1.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Helicase; Complete proteome.
SQ SEQUENCE 686 AA; 74505 MW; 6AAD7AA52B892A27 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 686;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 567 ADWDWA 572

RESULT 28
Q88NQ1      PRELIMINARY;      PRT;      861 AA.
AC
Q88NQ1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Sensory box protein.
GN PPI154.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=125334463;
RA Nelson K.E., Weiner C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Peterson D., Tran K., Moazzes A.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
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RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AE016778; AAN6779.1; -.
DR TIGR; PPI154; -.
DR GO; GO:0004871; F:signal transducer activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR007892; CHASE4.
DR InterPro; IPR001633; EAL.
DR InterPro; IPR000160; GGDEF.
DR InterPro; IPR001610; PAC.
DR InterPro; IPR000014; PAS_domain.
DR InterPro; IPR000437; ProK_lipoprot_S.
DR Pfam; PF00563; EAL; 1.
DR Pfam; PF005228; CHASE4; 1.
DR Pfam; PF00990; GGDEF; 1.
DR Pfam; PF00785; PAC; 1.
DR Pfam; PF00989; PAS; 1.
DR PROSITE; PS00883; EAL; 1.
DR PROSITE; PS00887; GGDEF; 1.
DR PROSITE; PS00112; PAS; 1.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Complete proteome.
SQ SEQUENCE 861 AA; 95980 MW; 64D652AFC7C3B9D6 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 861;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADWSWA 6
DB 91 ADQWA 96

RESULT 29
Q9AAZ6      PRELIMINARY;      PRT;      889 AA.
AC
Q9AAZ6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TonB-dependent receptor.
GN CC0446.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Niernan W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Uterback T., Iran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RC Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005717; AAK22433.1; -.
DR PIR; E87304; E87304.
DR TIGR; CC0446; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_dep_Rec; 1.
KW Receptor; Complete proteome.
SQ SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 889;
```

Best Local Similarity 100.0%; Pred. No. 1.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 ADMSW 5

Db 618 ADMSW 622

RESULT 30

Q9XGZ2 PRELIMINARY; PRT; 1005 AA.
ID Q9XGZ2
AC Q9XGZ2
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TIN24.22 protein (Putative receptor protein kinase).
GN TIN24.22 OR AT5G25930.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA WashU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana TIN24.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Huan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Iehida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF149413; AAD40144.1; -.
DR EMBL; BT004058; AAO42089.1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_pkin_AS.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase.
SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 ADMSW 5

Db 906 ADMSW 910

RESULT 31

Q820F9 PRELIMINARY; PRT; 1324 AA.
ID Q820F9
AC Q820F9
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative FtsK/spoIIIE family protein.
GN SAV5442.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AR005042; BAC73154.1; -.
DR GO; GO:0004182; F:carboxypeptidase A activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR InterPro; IPR000834; Peptidase_M14.
DR Pfam; PF01580; FtsK_SpoIIIE; 2.
DR SMART; SM00382; AAA; 3.
DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; 1.
DR PROSITE; PS0901; FTSK_SPOIIIE; 3.
KW Complete proteome.
SQ SEQUENCE 1324 AA; 143398 MW; 8E24138D58089456 CRC64;
Query Match 90.0%; Score 36; DB 16; Length 1324;
Best Local Similarity 83.3%; Pred. No. 1.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 ADMSW 6

Db 254 ADMSW 259

RESULT 32

Q9L4X2 PRELIMINARY; PRT; 5435 AA.
ID Q9L4X2
AC Q9L4X2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NybJ.

GN NYSU.
OS Streptomyces noursei.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1971;
RW [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11455; PubMed=10873841;
RX MEDLINE=20134850; Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,
RA Brutaaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,
RA Valla S., Zorchev S.B.;
RT "Biosynthesis of the polyene antifungal antibiotic nystatin in
Streptomyces noursei ATCC 11455: analysis of the gene cluster and
deduction of the biosynthetic pathway.";
RL Chem. Biol. 7:395-403(2000).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY. AAF71767.1; -.
CC EMBL; AF263912; AAF71767.1; -.
DR HSSP; P25715; IMLA.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0004314; F:lacyl-carrier protein S-malonyltransferase. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac trans.
DR InterPro; IPR002198; ADH_short.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR004410; Fabd.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR006163; Pp bind.
DR Pfam; PF00698; Acyl_transf; 3.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc N; 1.
DR Pfam; PF00109; ketoacyl-synt; 3.
DR Pfam; PF02801; ketoacyl-synt C; 3.
DR Pfam; PF00550; pp-binding; 3.
DR TIGRFAMs; TIGR00128; fabd; 3.
DR PROSITE; PS50075; ACP_DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.
DR PROSITE; PS00012; PHOSPHOPANTHETINE; 3.
KW Oxidoreductase; Phosphopantetheine; Transferase.
SQ SEQUENCE 5435 AA; 562659 MW; AA55465DF087A38C CRC64;

Query Match 90.0%; Score 36; DB 2; Length 5435;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1525 ADWSW 1529
|||||

RESULT 33
Q829Q9 PRELIMINARY; PRT; 527 AA.
AC Q829Q9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN SAV6350.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=33903;
RW [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis: deducing the ability of producing secondary
RT metabolites.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=22608306; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.;
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AP005046; BAC74061.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 527 AA; 57663 MW; B8E5D28F9CD77148 CRC64;

Query Match 87.5%; Score 35; DB 16; Length 527;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSW 6
Db 521 ADWFWA 526
|||||

RESULT 34
Q8NEW1 PRELIMINARY; PRT; 166 AA.
AC Q8NEW1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90714.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masubo Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075195; BAC11463.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR000379; Ser_estrs.
KW Hypothetical protein.
SQ SEQUENCE 166 AA; 18985 MW; 1C23AE4254636618 CRC64;

Query Match 85.0%; Score 34; DB 4; Length 166;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSW 6
Db 19 ASWSWA 24
|||||

RESULT 35
Q94JM4 PRELIMINARY; PRT; 273 AA.
ID Q94JM4;
AC Q94JM4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT4G19390/TSK18_170.

```
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Bann J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378856; AAK55659.1; -.
SQ SEQUENCE 273 AA; 30043 MW; BOCABDBE88971B3A CRC64;

Query Match 85.0%; Score 34; DB 10; Length 273;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 36
Q940D6 PRELIMINARY; PRT; 273 AA.
ID Q940D6
AC Q940D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AT4G19390/T5K18.170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY055785; AAL06921.1; -.
SQ SEQUENCE 273 AA; 30085 MW; 518FA9EFFD9D2003B CRC64;

Query Match 85.0%; Score 34; DB 10; Length 273;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 37
O65710 PRELIMINARY; PRT; 275 AA.
ID O65710
AC O65710;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
```

```
GN TSK18.170 OR AT4G19390.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.,
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Van Der Schueren J., Chuang Y.-J., Aert R., Defoor E., Robben J.,
RA Volckaert G., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL022580; CAA18626.1; -.
DR EMBL; AL161550; CAB78941.1; -.
DR PIR; T05822; T05822.
KW Hypothetical protein.
SQ SEQUENCE 275 AA; 30289 MW; 5157A10663950B62 CRC64;

Query Match 85.0%; Score 34; DB 10; Length 275;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 57 SDWSWS 62

RESULT 38
Q80UX8 PRELIMINARY; PRT; 337 AA.
ID Q80UX8
AC Q80UX8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE I110065L07R1k protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hoien L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

RC STRAIN=C57BL/6J; TISSUE=Breast tumor;
 RA Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC043690; AAH43690.1; -;
 DR GO; GO:0003824; F: catalytic activity; IEA.
 DR InterPro; IPR000379; Ser_estr.
 SQ SEQUENCE 337 AA; 38525 MW; 0BAA241B44567B09 CRC64;
 Query Match 85.0%; Score 34; DB 11; Length 337;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ADWSWA 6
 Db 19 ASWSWA 24
 RESULT 39
 Q9UVL4 PRELIMINARY; PRT; 376 AA.
 AC Q9UVL4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Polylacturonase (SC 3.2.1.15).
 GN PGGI.
 OS Penicillium griseoroseum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OC NCBI_taxid=84562;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=CCT 6421;
 RA Ribon A.O.B., D'Angelo M.A.C., Coelho J.L.C., Queiroz M.V.,
 RA Araujo E.F.;
 RT "Differential expression of polylacturonases genes from Penicillium griseoroseum";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES (POLYLACTURONASES).
 CC EMBL; AF195791; AAF06810.1; -;
 DR GO; GO:0005618; C: cell wall; IEA.
 DR GO; GO:0016798; F: hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0004650; F: polylacturonase activity; IEA.
 DR GO; GO:0005975; P: carbohydrate metabolism; IEA.
 DR InterPro; IPR000743; Glyco_hydro_28.
 DR InterPro; IPR006626; PbH1.
 DR Pfam; PF00295; Glyco_hydro_28; 1.
 DR SMART; SM00710; PbH1; 5.
 DR PROSITE; PS00502; POLYLACTURONASE; 1.
 KW Cell wall; Glycosidase; Hydrolase.
 SQ SEQUENCE 376 AA; 38038 MW; 0370737385B8C258 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 376;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
 Db 349 SDWSWS 354

RESULT 40
 P93050 PRELIMINARY; PRT; 617 AA.
 AC P93050;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE ATPK2324 (AT2G48010/T9J23.16).
 GN RKF3 OR T9J23.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 RN NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA C24;
 RA Kertbundit S., Linacero R., Rouze P., Galis I., Macas J., Deboeck F.,
 RA Hernalsteens J., De Greve H.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=COLUMBIA;
 RC Takahashi T., Mu J.-H., Gasch A., Chua N.-H.;
 RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RC Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.,
 RA Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Shinn P.,
 RA Tracy S.E., Banh J., Bowser L., Carninci P., Chung M.K.,
 RA Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Pham P.K., Quach H.L.,
 RA Sakano H., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C.,
 RA Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [5]
 RN SEQUENCE FROM N.A.
 RP Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Huan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones";
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; Z84202; CAB06335.1; -;
 DR EMBL; AF024650; AAC50045.1; -;
 DR EMBL; AC006072; AAD13705.1; -;
 DR EMBL; AY037237; AAK59837.1; -;
 DR EMBL; BT000518; AAN18087.1; -;
 DR PIR; C84922; C84922.
 DR HSP; P12931; IFMK.
 DR GO; GO:0005524; F: ATP binding; IEA.
 DR GO; GO:0003676; F: nucleic acid binding; IEA.
 DR GO; GO:0004674; F: protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F: protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F: transferase activity; IEA.
 DR GO; GO:0006468; P: protein amino acid phosphorylation; IEA.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR InterPro; IPR008271; Ser_thr_kin_AS.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.


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SQ SEQUENCE 617 AA; 67223 MW; 295D694B8563408A CRC64;
Query Match 85.0%; Score 34; DB 10; Length 617;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
|||:|:|
Db 500 ADMSWA 505

RESULT 41
Q8PU70 PRELIMINARY; PRT; 1074 AA.
AC Q8PU70;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Oar protein.
GN OAR OR XAC2672.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Fatah C.S., Furlan L.R.,
RA Quaggio R.B., Montelero-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A., L.P.,
RA Canarotte G., Cannavaro J., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorfy H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Fomighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463 (2002).
DR EMBL; AE011907; AAM37519.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008969; CarboxypepD_reg.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_dep_Reg; 1.
KW Complete proteome.
SQ SEQUENCE 1074 AA; 117359 MW; 7E949251E7D807C8 CRC64;
Query Match 85.0%; Score 34; DB 16; Length 1074;
Best Local Similarity 66.7%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
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Db 831 SDMSWS 836

RESULT 42
Q96WT6 PRELIMINARY; PRT; 1842 AA.
AC Q96WT6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fatty acid synthase alpha-subunit.
GN FAS2.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RC STRAIN=fas2/l8d1-H265;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fission yeast Schizosaccharomyces pombe fas2/l8d1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013749; BAB62031.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
```

```
DE Fatty acid synthase alpha-subunit.
GN FAS2.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RC STRAIN=fas2/l8d1-H518;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fission yeast Schizosaccharomyces pombe fas2/l8d1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013750; BAB62032.1; -.
DR PIR; A54083; A54083.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008278; 4-PPT_transf.
DR InterPro; IPR002582; ACPS.
DR InterPro; IPR000794; Ketoacyl_synth.
DR InterPro; IPR004568; Pantethn_trn.
DR InterPro; IPR006162; Ppantne_S.
DR Pfam; PF01648; ACPS; 1.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt_C; 1.
DR ProDom; PD004282; ACPS; 1.
DR TIGRFAMs; TIGR00556; pantethn_trn; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
KW Transferase.
SQ SEQUENCE 1842 AA; 202169 MW; E940DC93F2113676 CRC64;
Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
|||:|:|
Db 400 SDMSWA 405

RESULT 43
Q96WT7 PRELIMINARY; PRT; 1842 AA.
AC Q96WT7;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fatty acid synthase alpha-subunit.
GN FAS2.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RC STRAIN=fas2/l8d1-H265;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fission yeast Schizosaccharomyces pombe fas2/l8d1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013749; BAB62031.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
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DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR008278; 4-PPT_transf.
DR InterPro: IPR002582; ACPS.
DR InterPro: IPR000794; Ketoacyl_synth.
DR InterPro: IPR004568; Pantethn_trn.
DR InterPro: IPR006162; Ppantne_S.
DR Pfam: PF01648; ACPS; 1.
DR Pfam: PF01019; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt_C; 1.
DR ProDom: PD004282; ACPS; 1.
DR TIGRFAMs: TIGR00556; pantethn_trn; 1.
DR TrEMBL: F500606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; 1.
DR TRANSFERASE.
KW TRANSFERASE.
SQ SEQUENCE 1842 AA; 202138 MW; B8BF4D29C29E383B CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 400 SDMNWA 405

RESULT 44
Q96WT8 PRELIMINARY; PRT; 1842 AA.
ID Q96WT8
AC Q96WT8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR GO: fatty acid synthase alpha-subunit.
DR FAS2.
DR Schizosaccharomyces pombe (Fission Yeast).
DR Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
DR Schizosaccharomycetales; Schizosaccharomycetaceae;
DR Schizosaccharomycetes.
DR NCBI_TaxID=4896;
DR NCBI_TaxID=4896;
DR SEQUENCE FROM N.A.
RN [1]
RC STRAIN=fas2/lsl1-H201;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/lsl1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013748; BAB62030.1; -.
DR PIR; A54083; A54083.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR008278; 4-PPT_transf.
DR InterPro: IPR002582; ACPS.
DR InterPro: IPR000794; Ketoacyl_synth.
DR InterPro: IPR004568; Pantethn_trn.
DR InterPro: IPR006162; Ppantne_S.
DR Pfam: PF01648; ACPS; 1.
DR Pfam: PF01019; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt_C; 1.
DR ProDom: PD004282; ACPS; 1.
DR TIGRFAMs: TIGR00556; pantethn_trn; 1.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; 1.
DR TRANSFERASE.
KW TRANSFERASE.
SQ SEQUENCE 1842 AA; 202156 MW; F2F9612BEE3E316 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 400 SDMNWA 405

RESULT 44
Q96WT8 PRELIMINARY; PRT; 1842 AA.
ID Q96WT8
AC Q96WT8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR GO: fatty acid synthase alpha-subunit.
DR FAS2.
DR Schizosaccharomyces pombe (Fission Yeast).
DR Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
DR Schizosaccharomycetales; Schizosaccharomycetaceae;
DR Schizosaccharomycetes.
DR NCBI_TaxID=4896;
DR NCBI_TaxID=4896;
DR SEQUENCE FROM N.A.
RN [1]
RC STRAIN=fas2/lsl1-H201;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/lsl1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013748; BAB62030.1; -.
DR PIR; A54083; A54083.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR008278; 4-PPT_transf.
DR InterPro: IPR002582; ACPS.
DR InterPro: IPR000794; Ketoacyl_synth.
DR InterPro: IPR004568; Pantethn_trn.
DR InterPro: IPR006162; Ppantne_S.
DR Pfam: PF01648; ACPS; 1.
DR Pfam: PF01019; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt_C; 1.
DR ProDom: PD004282; ACPS; 1.
DR TIGRFAMs: TIGR00556; pantethn_trn; 1.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; 1.
DR TRANSFERASE.
KW TRANSFERASE.
SQ SEQUENCE 1842 AA; 202156 MW; F2F9612BEE3E316 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 400 SDMNWA 405

RESULT 44
Q96WT8 PRELIMINARY; PRT; 1842 AA.
ID Q96WT8
AC Q96WT8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR GO: fatty acid synthase alpha-subunit.
DR FAS2.
DR Schizosaccharomyces pombe (Fission Yeast).
DR Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
DR Schizosaccharomycetales; Schizosaccharomycetaceae;
DR Schizosaccharomycetes.
DR NCBI_TaxID=4896;
DR NCBI_TaxID=4896;
DR SEQUENCE FROM N.A.
RN [1]
RC STRAIN=fas2/lsl1-H201;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/lsl1.";
RL Biochim. Biophys. Acta 1532:223-233 (2001).
DR EMBL; AB013748; BAB62030.1; -.
DR PIR; A54083; A54083.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR008278; 4-PPT_transf.
DR InterPro: IPR002582; ACPS.
DR InterPro: IPR000794; Ketoacyl_synth.
DR InterPro: IPR004568; Pantethn_trn.
DR InterPro: IPR006162; Ppantne_S.
DR Pfam: PF01648; ACPS; 1.
DR Pfam: PF01019; ketoacyl-synt; 1.
DR Pfam: PF02801; ketoacyl-synt_C; 1.
DR ProDom: PD004282; ACPS; 1.
DR TIGRFAMs: TIGR00556; pantethn_trn; 1.
DR PROSITE: PS00606; B_KETOACYL_SYNTHASE; 1.
DR PROSITE: PS00012; PHOSPHOPANTHETINE; 1.
DR TRANSFERASE.
KW TRANSFERASE.
SQ SEQUENCE 1842 AA; 202156 MW; F2F9612BEE3E316 CRC64;

Query Match 85.0%; Score 34; DB 3; Length 1842;
Best Local Similarity 66.7%; Pred. No. 4.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 400 SDMNWA 405

RESULT 44
Q96WT8 PRELIMINARY; PRT; 1842 AA.
ID Q96WT8
AC Q96WT8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR GO: fatty acid synthase alpha-subunit.
DR FAS2.
DR Schizosaccharomyces pombe (Fission Yeast).
DR Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
DR Schizosaccharomycetales; Schizosaccharomycetaceae;
DR Schizosaccharomycetes.
DR NCBI_TaxID=4896;
DR NCBI_TaxID=4896;
DR SEQUENCE FROM N.A.
RN [1]
RC STRAIN=fas2/lsl1-H201;
RX MEDLINE=21363051; PubMed=11470243;
RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,
RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.;
RT "Very long-chain fatty-acid-containing phospholipids accumulate in
RT fatty acid synthase temperature-sensitive mutant strains of the
RT fission yeast Schizosaccharomyces pombe fas2/lsl1.";
RL Biochim. Biophys. Acta 1532:

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista A.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fobler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003760; AAF56698.1; -.
DR FlyBase; FBgn0040609; CG3348.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008061; P:chitin binding; IEA.
DR GO; GO:0006030; P:chitin metabolism; IEA.
DR InterPro; IPR002557; Chitin bind PezA.
SQ SEQUENCE 98 AA; 11343 MW; 4AD2AF1C2202BEE2 CRC64;

Query Match 82.5%; Score 33; DB 5; Length 98;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 75 ADWAW 79

RESULT 47
Q8KZ39 PRELIMINARY; PRT; 136 AA.
AC Q8KZ39;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Conserved hypothetical protein.
GN EBAC000-60D04.2.
OS uncultured proteobacterium.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=153809;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21822632; PubMed=11832943;
RA Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unsuspected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AE008921; AAM48635.1; -.
DR InterPro; IPR007628; DUF589.
DR Pfam; PF04543; DUF589; 1.
KW Hypothetical protein.
SQ SEQUENCE 136 AA; 15643 MW; D3CC7C550549AB2 CRC64;

Query Match 82.5%; Score 33; DB 2; Length 136;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 |||||

us-09-847-940c-6.rspt

Db 11 ATWSWA 16

RESULT 48
Q8BGD2 PRELIMINARY; PRT; 154 AA.
AC Q8BGD2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN A730061H03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK043157; BAC31480.1; -.
DR MGD; AK049078; BAC33535.1; -.
DR MGD; MGI:2445099; A730061H03RIK.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 154 AA; 16524 MW; A526724D4074D888 CRC64;

Query Match 82.5%; Score 33; DB 11; Length 154;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 9 ADWNW 13

RESULT 49
Q821K8 PRELIMINARY; PRT; 155 AA.
AC Q821K8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN CCA00932.
OS Chlamydomophila caviae.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
OX NCBI_TaxID=83557;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GPIC;
RX MEDLINE=225569155; PubMed=12682364;
RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
RA Unayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA Fraser C.M.;
RT "Genome sequence of Chlamydomophila caviae (Chlamydia psittaci GPIC):
RT examining the role of niche-specific genes in the evolution of the
RT Chlamydiaceae.";
RL Nucleic Acids Res. 31:2134-2147(2003).
DR EMBL; AE016997; AAP05671.1; -.
DR TIGR; CCA00932; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 155 AA; 17251 MW; 62B7907287D93DC8 CRC64;

Query Match 82.5%; Score 33; DB 16; Length 155;
Best Local Similarity 80.0%; Pred. No. 5.9e+02;

```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
|||:|
Db 90 ADWNW 94

RESULT 50
Q84UN9 PRELIMINARY; PRT; 159 AA.
AC O84UN9;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE B1027A11.9 protein.
GN B1027A11.9.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
clone:B1027A11.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF005464; BAC66742.1; "-".
SQ SEQUENCE 159 AA; 16692 MW; B3B044A8EA1C4427 CRC64;

Query Match 82.5%; Score 33; DB 10; Length 159;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
|||:
Db 80 DWAWA 84

Search completed: July 23, 2004, 13:19:28
Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:19:59 ; Search time 35 Seconds
(without alignments)
54.089 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADMSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTRMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	205	16	Q9ACR5
2	5	83.3	227	4	Q8IXK8
3	5	83.3	228	8	Q7YUG8
4	5	83.3	236	3	Q8NJY9
5	5	83.3	242	12	Q919K8
6	5	83.3	274	16	Q8G659
7	5	83.3	355	11	Q8BIT9
8	5	83.3	358	10	O50002
9	5	83.3	374	16	Q9HZ10
10	5	83.3	375	5	Q86KSO
11	5	83.3	426	5	Q86KFX
12	5	83.3	433	16	Q8P4A1
13	5	83.3	438	16	Q8PFV8
14	5	83.3	452	4	Q56AB7
15	5	83.3	463	5	Q8MMJ0
16	5	83.3	470	12	Q7TF27

17	5	83.3	477	11	Q9CYU6
18	5	83.3	484	4	Q8BTV6
19	5	83.3	581	5	Q8MSH3
20	5	83.3	597	5	Q9VGP2
21	5	83.3	605	16	Q82MX2
22	5	83.3	889	16	Q9AAZ6
23	5	83.3	1005	10	Q9XGZ2
24	5	83.3	5435	2	Q9L4X2
25	4	66.7	53	2	Q46496
26	4	66.7	54	8	Q9XPF8
27	4	66.7	57	10	Q84RU5
28	4	66.7	57	16	Q8YQ61
29	4	66.7	65	16	Q7UGI2
30	4	66.7	74	16	Q99QG6
31	4	66.7	76	6	Q862X5
32	4	66.7	77	16	Q7UUN4
33	4	66.7	77	16	Q7UGR5
34	4	66.7	82	16	Q7V158
35	4	66.7	85	16	Q8FBL8
36	4	66.7	87	9	Q8HAI2
37	4	66.7	88	16	Q97SD6
38	4	66.7	88	16	Q8CZ62
39	4	66.7	90	2	Q9F9Z5
40	4	66.7	92	10	Q8H6W2
41	4	66.7	93	2	Q939G8
42	4	66.7	94	10	Q39643
43	4	66.7	95	15	Q9YT75
44	4	66.7	96	16	Q7U4Q9
45	4	66.7	98	16	Q8AAB6
46	4	66.7	100	16	Q9JUR16
47	4	66.7	101	16	Q82UA8
48	4	66.7	101	16	Q8GSE6
49	4	66.7	101	16	Q7V3S8
50	4	66.7	103	12	Q68355
51	4	66.7	103	16	Q83LG1
52	4	66.7	106	3	P78996
53	4	66.7	107	9	Q853U1
54	4	66.7	108	2	Q68922
55	4	66.7	113	12	Q86624
56	4	66.7	118	9	Q9ZX36
57	4	66.7	118	16	Q8A5R3
58	4	66.7	118	16	Q89GGA
59	4	66.7	118	16	Q8X744
60	4	66.7	121	10	Q7XMX1
61	4	66.7	125	10	Q9ZP72
62	4	66.7	126	11	Q8C3P0
63	4	66.7	128	16	Q92RD9
64	4	66.7	128	16	Q9EX37
65	4	66.7	129	16	Q34882
66	4	66.7	130	2	Q9EV83
67	4	66.7	130	6	Q862Y3
68	4	66.7	131	11	Q9D2I8
69	4	66.7	131	15	P88067
70	4	66.7	131	16	Q98KA6
71	4	66.7	131	16	Q98GR5
72	4	66.7	133	2	Q47067
73	4	66.7	133	16	Q9K3M3
74	4	66.7	133	17	Q9HSB7
75	4	66.7	134	16	Q8UBK3
76	4	66.7	135	16	Q9I380
77	4	66.7	135	16	Q87211
78	4	66.7	136	2	Q8KZ39
79	4	66.7	136	16	Q8FRG4
80	4	66.7	137	17	Q9HSP0
81	4	66.7	140	4	Q86W69
82	4	66.7	140	13	Q8JIE5
83	4	66.7	140	17	Q97AQ3
84	4	66.7	143	5	Q22584
85	4	66.7	146	2	Q8RFQ2
86	4	66.7	146	8	Q9B5P8
87	4	66.7	146	16	Q81XE7
88	4	66.7	146	16	Q812K6
89	4	66.7	147	10	Q84T37

Q9CYU6	mus musculus
Q9BTV6	homo sapien
Q8MSH3	drosophila
Q9VGP2	drosophila
Q82MX2	streptomyce
Q9AAZ6	caulobacter
Q9XGZ2	arabidopsis
Q9L4X2	streptomyce
Q46496	desulfoarcu
Q9XPF8	gonostoma g
Q84RU5	oryza sativ
Q8YQ61	anabaena sp
Q7UGI2	rhodopirell
Q99QG6	streptomyce
Q862X5	bos taurus
Q7UUN4	rhodopirell
Q7UGR5	rhodopirell
Q7V158	prochloroco
Q8FBL8	escherichia
Q8HAI2	salmonella
Q97SD6	streptococc
Q8CZ62	streptococc
Q9F9Z5	serratia en
Q8H6W2	cicer ariet
Q939G8	pseudomonas
Q39643	cucumis sat
Q9YT75	human immun
Q7U4Q9	synchococcc
Q8AAB6	bacteroides
Q9JUR16	neisseria m
Q82UA8	nitrosomona
Q8GSE6	oryza sativ
Q7V3S8	prochloroco
Q68355	hepatitis c
Q83LG1	shigella fl
P78996	saccharomyc
Q853U1	mycobacteri
Q68922	streptomyce
Q86624	human herpe
Q9ZX36	mycobacteri
Q8A5R3	bacteroides
Q89GGA	bradyrhizob
Q8X744	escherichia
Q7XMX1	oryza sativ
Q9ZP72	schizosella
Q8C3P0	mus musculus
Q92RD9	rhizobium m
Q9EX37	streptomyce
Q34882	bacillus au
Q9EV83	pseudomonas
Q862Y3	bos taurus
Q9D2I8	mus musculus
P88067	human immun
Q98KA6	rhizobium l
Q98GR5	rhizobium l
Q47067	escherichia
Q9K3M3	streptomyce
Q9HSB7	halobacteri
Q8UBK3	agrobacteri
Q9I380	pseudomonas
Q87211	pseudomonas
Q8KZ39	uncultured
Q8FRG4	corynebacte
Q9HSP0	halobacteri
Q86W69	homo sapien
Q8JIE5	agalacthniis
Q97AQ3	thermoplasm
Q22584	caenorhabdi
Q8RFQ2	bacillus an
Q9B5P8	bipalium sp
Q81XE7	capillus an
Q812K6	capillus ce
Q84T37	oryza sativ

90	4	66.7	151	16	Q9JYQ4	Q9JYQ4 neisseria m	163	4	66.7	208	16	Q8REU4	Q8reu4 fusobacteri
91	4	66.7	152	15	Q9J6E9	Q9J6E9 human immun	164	4	66.7	210	2	Q84BA4	Q84ba4 erwinia chr
92	4	66.7	153	16	Q8YUC8	Q8YUC8 brucella me	165	4	66.7	210	5	Q9XUL5	Q9xul5 caenorhabdi
93	4	66.7	152	16	Q8FYH0	Q8fyh0 brucella su	166	4	66.7	210	16	Q9A684	Q9a684 caulobacter
94	4	66.7	153	17	O58545	O58545 pyrococcus	167	4	66.7	211	9	O80148	O80148 bacterioph
95	4	66.7	154	10	Q8LAJ1	Q8LAJ1 cucumis mel	168	4	66.7	211	9	O21903	O21903 bacterioph
96	4	66.7	154	10	Q8LK69	Q8LK69 cucumis sat	169	4	66.7	212	13	Q89WM0	Q89wm0 bradyrhizob
97	4	66.7	154	10	Q8LK96	Q8LK96 cucumis mel	170	4	66.7	212	16	Q89WM0	Q89wm0 bradyrhizob
98	4	66.7	154	10	Q8LK70	Q8LK70 cucumis sat	171	4	66.7	213	13	Q801Y7	Q801y7 brachydania
99	4	66.7	154	16	Q8LKT0	Q8LKT0 bacillus ce	172	4	66.7	213	16	Q82HK2	Q82hk2 streptomyce
100	4	66.7	155	10	Q8LSA9	Q8LSA9 cucumis sat	173	4	66.7	214	16	Q82K45	Q82k45 bacillus ha
101	4	66.7	155	11	Q7UTSQ4	Q7utsq4 arvicanthis	174	4	66.7	214	16	Q82K45	Q82k45 salmonella
102	4	66.7	156	16	Q88NT5	Q88nt5 pseudomonas	175	4	66.7	214	16	Q82L13	Q82l13 salmonella
103	4	66.7	160	16	Q8U535	Q8u535 agrobacteri	176	4	66.7	215	11	Q8VDR5	Q8vdr5 mus musculu
104	4	66.7	161	16	Q8A6Y5	Q8a6y5 bacteroides	177	4	66.7	215	11	Q8BTD1	Q8btd1 mus musculu
105	4	66.7	161	16	Q8A6Y5	Q8a6y5 bacteroides	178	4	66.7	216	2	Q8GEU0	Q8geu0 gamma-prote
106	4	66.7	163	10	O82086	O82086 zea mays (m	179	4	66.7	216	2	Q8GEU0	Q8geu0 gamma-prote
107	4	66.7	164	11	Q9EP94	Q9ep94 mus musculu	180	4	66.7	216	2	Q8SSZ2	Q8ssz2 sarcophaga
108	4	66.7	165	11	Q9CY62	Q9cy62 mus musculu	181	4	66.7	216	2	Q8SSZ2	Q8ssz2 sarcophaga
109	4	66.7	166	4	Q8NBW1	Q8nbw1 homo sapien	182	4	66.7	217	2	O52796	O52796 amycolatops
110	4	66.7	166	16	Q8Z5E0	Q8z5e0 salmonella	183	4	66.7	217	2	O52796	O52796 amycolatops
111	4	66.7	166	16	Q7WGX9	Q7wgx9 bordetella	184	4	66.7	218	15	P90011	P90011 human immun
112	4	66.7	166	16	Q7WGX9	Q7wgx9 bordetella	185	4	66.7	218	15	P90005	P90005 human immun
113	4	66.7	166	16	Q7VWA7	Q7vwa7 bordetella	186	4	66.7	218	15	P90019	P90019 human immun
114	4	66.7	168	4	Q96NQ0	Q96nq0 homo sapien	187	4	66.7	218	15	P90026	P90026 human immun
115	4	66.7	168	16	Q98K83	Q98k83 rhizobium l	188	4	66.7	218	15	P90066	P90066 human immun
116	4	66.7	169	5	Q9VKF4	Q9vkf4 drosophila	189	4	66.7	218	15	P90071	P90071 human immun
117	4	66.7	171	2	Q9FAY5	Q9fay5 pseudomonas	190	4	66.7	218	15	P90008	P90008 human immun
118	4	66.7	172	10	Q8LQJ4	Q8ljq4 prunus pers	191	4	66.7	218	15	P90008	P90008 human immun
119	4	66.7	175	5	Q9VBB9	Q9vbb9 drosophila	192	4	66.7	218	15	P90008	P90008 human immun
120	4	66.7	178	10	Q8LHJ6	Q8lhj6 oryza sativ	193	4	66.7	218	15	P90019	P90019 human immun
121	4	66.7	178	16	Q9HTL7	Q9htl7 pseudomonas	194	4	66.7	218	15	P90019	P90019 human immun
122	4	66.7	180	16	Q9H2B0	Q9hzb0 pseudomonas	195	4	66.7	218	15	P90023	P90023 human immun
123	4	66.7	180	16	Q98AC9	Q98ac9 rhizobium l	196	4	66.7	218	15	P90023	P90023 human immun
124	4	66.7	180	16	Q8P085	Q8pj85 xanthomonas	197	4	66.7	218	15	P90001	P90001 human immun
125	4	66.7	181	16	Q8EJ28	Q8ej28 shewanella	198	4	66.7	218	15	P90001	P90001 human immun
126	4	66.7	181	16	Q8EJ28	Q8ej28 shewanella	199	4	66.7	218	15	P90003	P90003 human immun
127	4	66.7	182	16	Q8P6I6	Q8p6i6 xanthomonas	200	4	66.7	218	15	P90009	P90009 human immun
128	4	66.7	185	16	Q88LD6	Q88ld6 pseudomonas	201	4	66.7	218	15	P90015	P90015 human immun
129	4	66.7	188	16	Q9CK28	Q9ckz8 pasteurella	202	4	66.7	218	15	P90018	P90018 human immun
130	4	66.7	188	16	Q92V87	Q92v87 rhizobium m	203	4	66.7	218	15	P90002	P90002 human immun
131	4	66.7	189	2	Q849H0	Q849h0 streptomyce	204	4	66.7	218	15	P90010	P90010 human immun
132	4	66.7	189	16	Q89VR9	Q89vr9 bradyrhizob	205	4	66.7	218	15	P90010	P90010 human immun
133	4	66.7	189	16	Q7WR37	Q7wr37 bordetella	206	4	66.7	218	15	P90012	P90012 human immun
134	4	66.7	189	16	Q7W271	Q7w271 bordetella	207	4	66.7	218	15	P90012	P90012 human immun
135	4	66.7	190	16	Q8Z7X5	Q8z7x5 salmonella	208	4	66.7	218	15	P90018	P90018 human immun
136	4	66.7	191	16	Q8PNV6	Q8pnv6 xanthomonas	209	4	66.7	218	15	P90014	P90014 human immun
137	4	66.7	191	17	Q29160	Q29160 archaeoglob	210	4	66.7	218	15	P90025	P90025 human immun
138	4	66.7	192	6	Q9BGX8	Q9bgx8 macaca fasc	211	4	66.7	218	15	P90025	P90025 human immun
139	4	66.7	192	10	Q7XVE3	Q7xve3 oryza sativ	212	4	66.7	218	15	P90024	P90024 human immun
140	4	66.7	193	16	Q835M7	Q835m7 enterococc	213	4	66.7	218	15	P90022	P90022 human immun
141	4	66.7	194	11	Q9EPC4	Q9epc4 mus musculu	214	4	66.7	218	15	P90000	P90000 human immun
142	4	66.7	194	16	Q9A7S1	Q9a7s1 caulobacter	215	4	66.7	218	15	P90021	P90021 human immun
143	4	66.7	195	4	Q96LM6	Q96lw6 homo sapien	216	4	66.7	218	15	P90000	P90000 human immun
144	4	66.7	195	16	Q87YI5	Q87yi5 pseudomonas	217	4	66.7	218	15	P90021	P90021 human immun
145	4	66.7	196	16	Q9A6I2	Q9a6i2 caulobacter	218	4	66.7	218	15	P90013	P90013 human immun
146	4	66.7	200	16	O54163	O54163 streptomyce	219	4	66.7	218	15	P90013	P90013 human immun
147	4	66.7	200	16	Q88XZ4	Q88xz4 lactobacill	220	4	66.7	218	15	P98074	P98074 human immun
148	4	66.7	201	16	Q82NK5	Q82nk5 streptomyce	221	4	66.7	218	15	P98076	P98076 human immun
149	4	66.7	203	2	Q9WMG7	Q9wmw7 pseudomonas	222	4	66.7	218	15	P90006	P90006 human immun
150	4	66.7	203	16	O51366	O51366 borrelia bu	223	4	66.7	218	15	P90016	P90016 human immun
151	4	66.7	204	16	Q51367	Q51367 borrelia bu	224	4	66.7	218	15	P90007	P90007 human immun
152	4	66.7	204	16	Q7VZD0	Q7vzd0 bordetella	225	4	66.7	218	15	P98069	P98069 human immun
153	4	66.7	205	5	Q7YVW0	Q7yvw0 caenorhabdi	226	4	66.7	219	16	P98068	P98068 human immun
154	4	66.7	205	16	O69756	O69756 pseudomonas	227	4	66.7	223	4	Q8WT3	Q8wt3 ralestonia s
155	4	66.7	206	16	Q9PBA5	Q9pba5 xylella fas	228	4	66.7	223	5	Q8WJ3	Q8wj3 rhodospira
156	4	66.7	206	16	Q9HV17	Q9hvl17 pseudomonas	229	4	66.7	223	5	Q8WJ3	Q8wj3 rhodospira
157	4	66.7	206	16	Q8RTK1	Q8rtk1 xanthomonas	230	4	66.7	223	5	Q8WJ3	Q8wj3 rhodospira
158	4	66.7	206	16	Q8PMV6	Q8pmv6 xanthomonas	231	4	66.7	223	5	Q8WJ3	Q8wj3 rhodospira
159	4	66.7	206	16	Q87C12	Q87cl2 xylella fas	232	4	66.7	223	5	Q8WJ3	Q8wj3 rhodospira
160	4	66.7	207	5	Q27449	Q27449 brugia mala	233	4	66.7	224	16	Q81XU7	Q81xu7 bacillus an
161	4	66.7	207	9	O80124	O80124 bacterioph	234	4	66.7	225	10	Q9LI49	Q9li49 oryza sativ
162	4	66.7	207	9	Q858N9	Q858n9 lactococcus	235	4	66.7	225	11	Q8R2Z2	Q8r2z2 mus musculu

236	4	66.7	225	11	Q9DJJ5	Q9dlj5 mus musculus	309	4	66.7	257	16	Q89GU8	Q89gu8 bradyrhizob
237	4	66.7	225	11	Q8VCR5	Q8vcr5 mus musculus	310	4	66.7	258	10	Q8FG08	Q8fg08 arabidopsis
238	4	66.7	227	16	Q9KXS7	Q9kxs7 streptomyce	311	4	66.7	258	10	Q8H4P3	Q8h4p3 oryza sativ
239	4	66.7	227	16	Q87XG3	Q87xg3 pseudomonas	312	4	66.7	260	16	Q914A3	Q914a3 pseudomonas
240	4	66.7	228	2	Q8KX72	Q8kx72 rhodococcus	313	4	66.7	261	2	Q9AQG7	Q9aqg7 caldicellul
241	4	66.7	228	2	Q9L639	Q9l639 prochloroco	314	4	66.7	261	16	Q55715	Q55715 synecocyst
242	4	66.7	228	16	Q8EL80	Q8el80 oceanobacil	315	4	66.7	261	16	Q829X4	Q829x4 streptomyce
243	4	66.7	228	16	Q8EF09	Q8ef09 shewanella	316	4	66.7	262	2	Q8KZ64	Q8kz64 uncultured
244	4	66.7	228	16	Q7V1B1	Q7v1b1 prochloroco	317	4	66.7	262	16	Q8DAU8	Q8da8 vibrio vuln
245	4	66.7	230	16	Q8XYP2	Q8xyp2 ralatonia s	318	4	66.7	262	16	Q7U3N7	Q7u3n7 synecococ
246	4	66.7	230	16	Q8PRE3	Q8pre3 xanthomonas	319	4	66.7	263	10	Q9FR36	Q9fr36 glycine max
247	4	66.7	230	16	Q8PEG2	Q8peg2 xanthomonas	320	4	66.7	263	11	Q9BPB6	Q9ebp6 mus musculu
248	4	66.7	232	5	Q8INX8	Q8inx8 drosophila	321	4	66.7	263	11	Q9QZY1	Q9qzy1 mus musculu
249	4	66.7	232	16	Q8XPW6	Q8xpw6 ralatonia s	322	4	66.7	263	16	Q9AAP8	Q9aap8 caulobacter
250	4	66.7	232	16	Q82JK5	Q82jk5 streptomyce	323	4	66.7	266	5	Q9TZ29	Q9tzz9 caenorhabdi
251	4	66.7	232	16	Q82CK9	Q82ck9 streptomyce	324	4	66.7	266	5	Q94Z85	Q94z85 caenorhabdi
252	4	66.7	233	3	Q9C172	Q9c172 beauveria b	325	4	66.7	266	16	Q86750	Q86750 streptomyce
253	4	66.7	233	16	Q7VCF4	Q7vcf4 prochloroco	326	4	66.7	267	16	Q89CD4	Q89cd4 bradyrhizob
254	4	66.7	234	16	Q8P8F7	Q8p8f7 xanthomonas	327	4	66.7	268	16	Q7UF94	Q7uf94 rhodopirell
255	4	66.7	234	16	Q9X8P7	Q9x8p7 streptomyce	328	4	66.7	269	4	Q8NE88	Q8ne88 homo sapien
256	4	66.7	235	13	Q7Z294	Q7z294 brachydanio	329	4	66.7	272	4	Q8N712	Q8n712 homo sapien
257	4	66.7	236	2	Q08385	Q08385 rhodobacter	330	4	66.7	272	5	Q8MTV2	Q8mtv2 drosophila
258	4	66.7	236	2	Q9LAJ4	Q9laj4 rhodospiril	331	4	66.7	272	16	Q99XX1	Q99xx1 streptococ
259	4	66.7	236	5	Q8I859	Q8i859 drosophila	332	4	66.7	272	16	Q8K5R2	Q8k5r2 streptococ
260	4	66.7	237	3	Q8NJY2	Q8njy2 aspergillus	333	4	66.7	273	10	Q94JM4	Q94jm4 arabidopsis
261	4	66.7	238	16	Q8EM85	Q8em85 oceanobacil	334	4	66.7	273	10	Q94OD6	Q94od6 arabidopsis
262	4	66.7	239	16	Q9A5L5	Q9a5l5 caulobacter	335	4	66.7	273	16	Q9K152	Q9k152 neisseria m
263	4	66.7	239	16	Q98LF5	Q98lf5 rhizobium l	336	4	66.7	273	16	Q9JSS7	Q9jss7 neisseria m
264	4	66.7	240	3	Q8NJZ1	Q8njz1 rhinectria	337	4	66.7	273	16	Q8NZAL	Q8nza1 streptococ
265	4	66.7	240	5	Q86HE2	Q86he2 dictyosteli	338	4	66.7	273	16	Q8DS06	Q8ds06 streptococ
266	4	66.7	240	16	Q9PFU7	Q9pfu7 xylella fas	339	4	66.7	275	2	Q8KLX7	Q8klx7 pseudomonas
267	4	66.7	240	16	Q8YCS1	Q8ycs1 brucella me	340	4	66.7	275	10	Q65710	Q65710 arabidopsis
268	4	66.7	240	16	Q8FVK4	Q8fvk4 brucella su	341	4	66.7	275	12	Q7TGA4	Q7tga4 equine arte
269	4	66.7	240	16	Q87B76	Q87b76 xylella fas	342	4	66.7	275	12	Q7TGA2	Q7tga2 equine arte
270	4	66.7	241	2	Q9AKM2	Q9akm2 rickettsia	343	4	66.7	275	12	Q7TGA1	Q7tga1 equine arte
271	4	66.7	241	2	Q9AKG6	Q9akg6 rickettsia	344	4	66.7	275	12	Q7TGA0	Q7tga0 equine arte
272	4	66.7	241	16	Q92IJ8	Q92ij8 rickettsia	345	4	66.7	275	12	Q7TGG9	Q7tgg9 equine arte
273	4	66.7	242	3	Q9P8A6	Q9p8a6 agaricus bi	346	4	66.7	275	12	Q7TGG8	Q7tgg8 equine arte
274	4	66.7	242	5	Q8IGP9	Q8igp9 drosophila	347	4	66.7	276	16	Q9PD11	Q9pd11 xylella fas
275	4	66.7	242	10	Q8GT53	Q8gt53 hordeum vul	348	4	66.7	276	16	Q9PCS9	Q9pcs9 xylella fas
276	4	66.7	243	16	Q9JYR4	Q9jyr4 neisseria m	349	4	66.7	276	16	Q9CDA2	Q9cda2 mycobacteri
277	4	66.7	243	16	Q8YCL1	Q8ycl1 brucella me	350	4	66.7	276	16	Q877P0	Q877p0 xylella fas
278	4	66.7	243	16	Q7UTZ6	Q7utz6 rhodopirell	351	4	66.7	276	16	Q7UTG7	Q7utg7 rhodopirell
279	4	66.7	244	4	Q81VB3	Q81vb3 homo sapien	352	4	66.7	277	2	Q8GLB8	Q8glb8 xanthomonas
280	4	66.7	244	16	Q83GD4	Q83gd4 enterococcu	353	4	66.7	277	16	Q8UFC2	Q8ufc2 agrobacteri
281	4	66.7	245	16	Q92KJ4	Q92kj4 rhizobium m	354	4	66.7	277	16	Q92QE0	Q92qe0 rhizobium m
282	4	66.7	246	5	Q9UAV4	Q9uav4 caenorhabdi	355	4	66.7	277	16	Q88XJ0	Q88xj0 lactobacill
283	4	66.7	246	16	Q8E308	Q8e308 streptococ	356	4	66.7	278	16	P74248	P74248 synecocyst
284	4	66.7	246	16	Q8DX86	Q8dx86 streptococ	357	4	66.7	280	13	Q8UYV9	Q8uyv9 brachydanio
285	4	66.7	246	16	Q8CWD6	Q8cwd6 escherichia	358	4	66.7	280	16	Q8YW13	Q8ywi3 anabaena ep
286	4	66.7	246	16	Q87VQ5	Q87vg5 pseudomonas	359	4	66.7	280	16	P72049	P72049 mycobacteri
287	4	66.7	246	16	Q83DC4	Q83dc4 coxiella bu	360	4	66.7	280	16	Q7TVN9	Q7tvn9 mycobacteri
288	4	66.7	247	5	Q9VEZ4	Q9vez4 drosophila	361	4	66.7	280	16	Q7TTZ6	Q7ttz6 rhodopirell
289	4	66.7	247	16	Q97P63	Q97p63 streptococ	362	4	66.7	281	2	Q30796	Q30796 methylobact
290	4	66.7	247	16	Q8DS03	Q8ds03 streptococ	363	4	66.7	282	5	Q9BL05	Q9bl05 caenorhabdi
291	4	66.7	249	16	Q99XW9	Q99xw9 streptococ	364	4	66.7	282	16	Q8X7K0	Q8x7k0 escherichia
292	4	66.7	249	16	Q8NZ99	Q8nz99 streptococ	365	4	66.7	282	16	Q8FG09	Q8fg09 escherichia
293	4	66.7	249	16	Q8KSR0	Q8ksr0 streptococ	366	4	66.7	282	16	Q83QZ3	Q83qz3 shigella fl
294	4	66.7	249	16	Q7ULK2	Q7ulk2 rhodopirell	367	4	66.7	284	2	Q9R9Y3	Q9r9y3 pseudomonas
295	4	66.7	250	1	Q9P9C3	Q9p9c3 uncultured	368	4	66.7	284	16	Q9KJX7	Q9kjx7 pseudomonas
296	4	66.7	250	10	Q9XGG6	Q9xgg6 pisum sativ	369	4	66.7	285	4	Q9BUI3	Q9bui3 homo sapien
297	4	66.7	250	16	Q8PEX6	Q8pex6 xanthomonas	370	4	66.7	285	4	Q9NXI3	Q9nxi3 homo sapien
298	4	66.7	250	16	Q8NR79	Q8nr79 corynebacte	371	4	66.7	285	16	Q8XTZ3	Q8xtz3 ralatonia s
299	4	66.7	250	17	Q8TUH9	Q8tuh9 methanosarc	372	4	66.7	286	16	Q9KEF2	Q9kef2 bacillus ha
300	4	66.7	251	10	Q9LKL9	Q9lkl9 vitis berla	373	4	66.7	287	2	Q30655	Q30655 azotobacter
301	4	66.7	251	10	Q7XXR0	Q7xxr0 oryza sativ	374	4	66.7	289	16	Q8ZNO5	Q8zng5 salmonella
302	4	66.7	251	16	Q8DNP5	Q8dnp5 streptococ	375	4	66.7	289	16	Q8Z5G0	Q8z5g0 salmonella
303	4	66.7	251	16	Q8PNP3	Q8pn32 xanthomonas	376	4	66.7	289	16	Q8JTS9	Q8jts9 salmonella
304	4	66.7	255	16	Q7W1J7	Q7w1j7 bordetella	377	4	66.7	290	2	Q59078	Q59078 alteromonas
305	4	66.7	255	16	Q7W849	Q7w849 bordetella	378	4	66.7	290	12	Q88899	Q88899 tobacco rat
306	4	66.7	255	16	Q7VX82	Q7vx82 bordetella	379	4	66.7	291	11	Q811J1	Q811j1 mus musculu
307	4	66.7	256	2	Q9L9V0	Q9l9v0 chromatium	380	4	66.7	292	5	Q7VYN6	Q7vyn6 trypanosoma
308	4	66.7	257	16	Q9X787	Q9x787 mycobacteri	381	4	66.7	292	16	Q92VR3	Q92vr3 rhizobium m

382	4	66.7	292	16	Q8RJR5	Q89rj5 bradyrhizob	455	4	66.7	325	2	Q8VQC9	Q8vqc9 myxococcus
383	4	66.7	293	10	Q93V35	Q93v35 oryza sativ	456	4	66.7	325	2	Q8RMH1	Q8rmh1 acetobacter
384	4	66.7	293	10	Q7XKG4	Q7xkg4 oryza sativ	457	4	66.7	325	5	Q17095	Q17095 caenorhabdi
385	4	66.7	293	16	Q9A7P0	Q9a7p0 caulobacter	458	4	66.7	325	16	Q8DSQ6	Q8dsq6 streptococc
386	4	66.7	293	16	Q9EWV0	Q9ewv0 streptomyc	459	4	66.7	325	16	Q89DB4	Q89db4 bradyrhizob
387	4	66.7	293	16	Q7U5G6	Q7u5g6 synecococc	460	4	66.7	328	4	Q9UJ71	Q9uj71 homo sapien
388	4	66.7	294	16	Q9KVV5	Q9kvv5 vibrio chol	461	4	66.7	328	16	Q9WXR6	Q9wxr6 thermotoga
389	4	66.7	295	4	Q86VCS	Q86vc0 homo sapien	462	4	66.7	328	16	Q8DBH2	Q8dbh2 vibrio vuln
390	4	66.7	295	4	Q86VC0	Q86vc0 homo sapien	463	4	66.7	328	16	Q7UT80	Q7ut80 rhodopirell
391	4	66.7	295	11	Q9CV13	Q9cy13 mus musculu	464	4	66.7	328	16	Q7UMG3	Q7umg3 rhodopirell
392	4	66.7	295	11	Q91V31	Q91v31 m 13 days e	465	4	66.7	330	2	P72440	P72440 streptocov
393	4	66.7	295	16	Q883H4	Q883h4 pseudomonas	466	4	66.7	330	13	Q7ZW50	Q7zw50 brachydanio
394	4	66.7	295	16	Q881Y6	Q881y6 bacillus an	467	4	66.7	330	16	Q989M8	Q989m8 rhizobium l
395	4	66.7	295	16	Q81324	Q81324 bacillus ce	468	4	66.7	330	16	Q926E3	Q926e3 rhizobium m
396	4	66.7	295	2	Q52689	Q52689 rhodobacter	469	4	66.7	330	16	Q9KYH6	Q9kyh6 streptomyc
397	4	66.7	297	2	Q30730	Q30730 rhodobacter	470	4	66.7	331	16	Q833W8	Q833w8 enterococcu
398	4	66.7	297	11	Q8BG50	Q8bg50 mus musculu	471	4	66.7	331	16	Q7UW49	Q7uw49 rhodopirell
399	4	66.7	297	16	Q98B17	Q98b17 rhizobium l	472	4	66.7	332	2	Q8P5R6	Q8p5r6 streptomyc
400	4	66.7	298	2	Q8KP31	Q8kp31 agromyces m	473	4	66.7	332	5	Q9W2Q2	Q9w2q2 drosophila
401	4	66.7	298	16	Q9A9G2	Q9a9g2 caulobacter	474	4	66.7	332	8	Q9T7K6	Q9t7k6 crassostrea
402	4	66.7	298	16	Q83JN0	Q83jn0 shigella fl	475	4	66.7	332	10	Q93ZH9	Q93zh9 arabidopsis
403	4	66.7	299	10	Q9LM13	Q9lm13 arabidopsis	476	4	66.7	332	16	Q8PPH2	Q8pph2 xanthomonas
404	4	66.7	299	16	Q7V6D1	Q7v6d1 prochloroco	477	4	66.7	332	16	Q8P5D0	Q8p5d0 xanthomonas
405	4	66.7	300	2	Q59248	Q59248 bacillus su	478	4	66.7	332	16	Q87AY2	Q87ay2 xylella fas
406	4	66.7	300	6	Q9GMP3	Q9gmp3 macaca fasc	479	4	66.7	333	5	Q9W2J6	Q9w2j6 drosophila
407	4	66.7	300	16	Q9A237	Q9a237 caulobacter	480	4	66.7	334	10	Q84MQ0	Q84mq0 oryza sativ
408	4	66.7	300	16	Q96688	Q96688 bacillus su	481	4	66.7	334	16	Q92B16	Q92by6 streptomyc
409	4	66.7	301	16	Q98F65	Q98f65 rhizobium l	482	4	66.7	334	16	Q82FJ3	Q82fj3 streptomyc
410	4	66.7	302	10	Q8LJW6	Q8ljw6 sorghum bic	483	4	66.7	334	16	Q989F6	Q989f6 rhizobium l
411	4	66.7	302	16	Q9I670	Q9i670 pseudomonas	484	4	66.7	335	16	Q96KQ0	Q96kq0 homo sapien
412	4	66.7	302	16	Q8FYS1	Q8fys1 brucella su	485	4	66.7	336	4	Q92GH3	Q92gh3 streptomyc
413	4	66.7	303	10	Q9MLK7	Q9mlk7 arabidopsis	486	4	66.7	337	2	Q92GH3	Q92gh3 streptomyc
414	4	66.7	304	5	Q9XUN0	Q9xun0 caenorhabdi	487	4	66.7	337	5	P92001	P92001 caenorhabdi
415	4	66.7	304	16	Q8FDN3	Q8fdn3 escherichia	488	4	66.7	337	11	Q80UX8	Q8oux8 mus musculu
416	4	66.7	305	16	Q88RH3	Q88rh3 pseudomonas	489	4	66.7	337	16	Q7U531	Q7u531 rhodopirell
417	4	66.7	306	3	Q10186	Q10186 kluyveromyc	490	4	66.7	338	16	Q9RT55	Q9rt55 deinococcus
418	4	66.7	306	13	Q7ZX07	Q7zx07 xenopus lae	491	4	66.7	338	16	Q8XDE0	Q8xde0 escherichia
419	4	66.7	307	16	Q87U52	Q87u52 pseudomonas	492	4	66.7	338	16	P73085	P73085 synecocyst
420	4	66.7	307	16	Q8X9S5	Q8x9s5 streptomyc	493	4	66.7	338	16	P73085	P73085 synecocyst
421	4	66.7	307	16	Q8YJ28	Q8yj28 brucella me	494	4	66.7	339	5	P92002	P92002 caenorhabdi
422	4	66.7	307	16	Q830F5	Q830f5 enterococcu	495	4	66.7	340	16	Q9PGB5	Q9pgb5 xylella fas
423	4	66.7	308	2	Q93R73	Q93r73 streptococc	496	4	66.7	340	16	Q8KIP8	Q8kip8 pseudomonas
424	4	66.7	308	4	Q7Z6L3	Q7z6l3 homo sapien	497	4	66.7	341	2	Q8KIP8	Q8kip8 pseudomonas
425	4	66.7	308	13	Q803P6	Q803p6 brachydanio	498	4	66.7	341	16	Q882G1	Q882g1 agrobacteri
426	4	66.7	309	4	Q8N2Y4	Q8n2y4 homo sapien	499	4	66.7	342	16	Q8UKL8	Q8ukl8 streptomyc
427	4	66.7	309	16	Q8N2Y4	Q8n2y4 streptococc	500	4	66.7	342	16	P72464	P72464 streptomyc
428	4	66.7	310	2	Q9XBS7	Q9xbs7 zymomonas m	501	4	66.7	343	2	Q8KWC9	Q8kwc9 ruegeria sp
429	4	66.7	310	3	Q8TGE0	Q8tge0 aspergillus	502	4	66.7	343	2	Q8KWC9	Q8kwc9 ruegeria sp
430	4	66.7	310	10	Q84924	Q84924 sea mays (m	503	4	66.7	343	2	Q94LD0	Q94ld0 oryza sativ
431	4	66.7	312	16	Q8XZ21	Q8xz21 raiistoncia s	504	4	66.7	343	10	Q9SKL5	Q9skl5 arabidopsis
432	4	66.7	312	16	Q8N2P6	Q8n2p6 streptococc	505	4	66.7	344	16	Q32258	Q32258 bacillus su
433	4	66.7	313	16	Q8KG37	Q8kg37 chlorobium	506	4	66.7	344	16	Q7U660	Q7u660 synecococc
434	4	66.7	313	16	Q88T79	Q88t79 lactobacill	507	4	66.7	344	17	Q8TII4	Q8tii4 methanosarc
435	4	66.7	314	2	Q9AML6	Q9aml6 edwardsiell	508	4	66.7	345	2	Q9F620	Q9f620 rhizobium m
436	4	66.7	314	11	Q8BUX9	Q8bux9 mus musculu	509	4	66.7	345	10	Q8S9T8	Q8s9t8 oryza sativ
437	4	66.7	314	16	Q8FWA9	Q8fwa9 brucella su	510	4	66.7	345	16	Q92RZ1	Q92rz1 rhizobium m
438	4	66.7	315	16	Q87V43	Q87v43 pseudomonas	511	4	66.7	345	16	Q8YGG2	Q8ygg2 brucella me
439	4	66.7	316	2	Q69348	Q69348 rhodococcus	512	4	66.7	345	16	Q8G1F9	Q8g1f9 rhizobium l
440	4	66.7	317	11	Q8VBW9	Q8vbw9 mus musculu	513	4	66.7	345	16	Q8GT84	Q8gt84 lactobacill
441	4	66.7	317	16	Q55809	Q55809 synecocyst	514	4	66.7	346	2	Q8K190	Q8k190 edwardsiell
442	4	66.7	317	16	Q55809	Q55809 synecocyst	515	4	66.7	346	2	Q32484	Q32484 enterobacte
443	4	66.7	318	2	Q53813	Q53813 shigella bo	516	4	66.7	346	2	Q32484	Q32484 enterobacte
444	4	66.7	319	3	Q94064	Q94064 candida alb	517	4	66.7	346	2	Q848V3	Q848v3 edwardsiell
445	4	66.7	320	16	Q8NTB5	Q8ntb5 corynebacte	518	4	66.7	346	2	Q83WB5	Q83wb5 edwardsiell
446	4	66.7	320	2	Q84BJ7	Q84bj7 halobacilli	519	4	66.7	346	16	Q986J8	Q986j8 rhizobium l
447	4	66.7	321	4	Q86VE5	Q86ve5 homo sapien	520	4	66.7	346	16	Q92T78	Q92t78 rhizobium m
448	4	66.7	321	16	Q8U6Y1	Q8u6y1 agrobacteri	521	4	66.7	346	16	Q8ZKX5	Q8zqx5 salmonella
449	4	66.7	322	16	Q8PK81	Q8pk81 xanthomonas	522	4	66.7	346	16	Q8XBO3	Q8xb03 escherichia
450	4	66.7	323	12	Q9QTE2	Q9qte2 marek's dis	523	4	66.7	346	16	Q8CVJ8	Q8cvj8 escherichia
451	4	66.7	323	16	Q8XQW6	Q8xqw6 raiistoncia s	524	4	66.7	347	10	Q8Z2P5	Q8z2p5 salmonella
452	4	66.7	324	16	Q8YD70	Q8yd70 brucella me	525	4	66.7	347	17	Q29274	Q29274 archaeoglob
453	4	66.7	324	16	Q8FV61	Q8fv61 brucella su	526	4	66.7	349	16	Q8DSD3	Q8dsd3 streptococc
454	4	66.7	324	16	Q7U7Y6	Q7u7y6 synecococc	527	4	66.7	350	2	Q9RN58	Q9rn58 streptomyc

528	4	66.7	350	16	Q9LJB2	Q9L1B2 streptomyc	601	4	66.7	400	16	Q887E6	Q887e6 pseudomonas
529	4	66.7	351	5	Q13539	Q13539 homo sapien	602	4	66.7	400	16	Q82GL5	Q82gl5 streptomyc
530	4	66.7	351	5	Q95X33	Q95X33 caenorhabdi	603	4	66.7	400	16	Q7UTG5	Q7utg5 rhodopirell
531	4	66.7	351	16	Q8P543	Q8P543 xanthomonas	604	4	66.7	401	16	Q8G1G9	Q8g1g9 bruceella au
532	4	66.7	352	16	Q8P543	Q8P543 bradyrhizob	605	4	66.7	401	16	Q8FRT5	Q8ftr5 corynebacte
533	4	66.7	354	16	Q9HV16	Q9HV16 pseudomonas	606	4	66.7	403	5	Q61866	Q61866 caenorhabdi
534	4	66.7	355	16	Q9P314	Q9P314 streptomyc	607	4	66.7	404	2	Q9XSR5	Q9xs5 streptomyc
535	4	66.7	355	16	Q7UM56	Q7UM56 rhodopirell	608	4	66.7	404	10	Q94HM3	Q94hm3 oryza sativ
536	4	66.7	356	16	Q8DB65	Q8DB65 vibrio vuln	609	4	66.7	404	10	Q7XG17	Q7xg17 oryza sativ
537	4	66.7	357	2	Q9R8K8	Q9R8K8 xanthomonas	610	4	66.7	404	16	Q06263	Q06263 mycobacteri
538	4	66.7	357	2	Q83X88	Q83X88 xanthomonas	611	4	66.7	404	16	Q8G4W6	Q8g4w6 bifidobacte
539	4	66.7	357	13	Q7ZTN3	Q7ZTN3 xenopus lae	612	4	66.7	404	16	Q7TWH6	Q7twh6 mycobacteri
540	4	66.7	357	16	Q8PQC2	Q8PQC2 xanthomonas	613	4	66.7	405	5	Q93789	Q93789 caenorhabdi
541	4	66.7	357	16	Q8PB93	Q8PB93 xanthomonas	614	4	66.7	405	13	Q8UWH2	Q8uwh2 brachydanio
542	4	66.7	358	10	Q8LJ33	Q8LJ33 oryza sativ	615	4	66.7	408	16	Q7WM51	Q7wm51 bordetella
543	4	66.7	358	13	Q9YH17	Q9YH17 gallus gall	616	4	66.7	409	10	Q9M3F6	Q9m3f6 arabidopsis
544	4	66.7	358	16	Q89PW3	Q89PW3 bradyrhizob	617	4	66.7	410	16	Q7WK41	Q7wk41 bordetella
545	4	66.7	359	2	Q9K30	Q9K30 xanthomonas	618	4	66.7	410	16	Q7W8T1	Q7w8t1 bordetella
546	4	66.7	360	2	Q50378	Q50378 mycobacteri	619	4	66.7	410	16	Q7VZ32	Q7vz32 bordetella
547	4	66.7	360	10	Q9SHX9	Q9SHX9 arabidopsis	620	4	66.7	410	16	Q7V682	Q7v682 prochloroco
548	4	66.7	360	11	Q8CGB8	Q8CGB8 mus musculu	621	4	66.7	411	5	Q94252	Q94252 caenorhabdi
549	4	66.7	361	16	Q8CP95	Q8CP95 xanthomonas	622	4	66.7	411	16	Q8U9U2	Q8u9u2 agrobacteri
550	4	66.7	364	6	Q77568	Q77568 salmirel sci	623	4	66.7	411	16	Q92SC3	Q92sc3 rhizobium m
551	4	66.7	364	16	Q55548	Q55548 synchocyst	624	4	66.7	411	16	Q9RD79	Q9rd79 streptomyc
552	4	66.7	365	3	Q12231	Q12231 saccharomyc	625	4	66.7	415	10	Q9SIX0	Q9siox0 arabidopsis
553	4	66.7	369	10	Q8VWX2	Q8VWX2 perilla fru	626	4	66.7	415	13	Q7SXU1	Q7sxu1 brachydanio
554	4	66.7	369	16	Q8G7G2	Q8G7G2 bifidobacte	627	4	66.7	415	16	Q82002	Q82002 anabaena sp
555	4	66.7	371	16	Q9EX41	Q9EX41 streptomyc	628	4	66.7	415	16	Q7UWB0	Q7uwb0 rhodopirell
556	4	66.7	371	17	Q28901	Q28901 archaeoglob	629	4	66.7	416	16	Q7U9Q8	Q7u9q8 synchococc
557	4	66.7	372	5	Q23849	Q23849 dictyosteli	630	4	66.7	417	5	Q8INJ5	Q8inj5 drosophila
558	4	66.7	372	16	Q72682	Q72682 synchocyst	631	4	66.7	417	16	Q53319	Q53319 mycobacteri
559	4	66.7	373	16	Q9ZC00	Q9ZC00 streptomyc	632	4	66.7	419	16	Q982K3	Q982k3 rhizobium 1
560	4	66.7	373	16	Q8FQAS	Q8FQAS corynebacte	633	4	66.7	419	16	Q9WZ64	Q9wz64 thermotoga
561	4	66.7	374	2	Q9X471	Q9X471 streptomyc	634	4	66.7	420	6	Q95K62	Q95k62 macaca fasc
562	4	66.7	374	16	Q7TX42	Q7TX42 mycobacteri	635	4	66.7	421	5	Q9GPA6	Q9gpa6 strongyloce
563	4	66.7	375	17	Q8ZS69	Q8ZS69 pyrobaculum	636	4	66.7	421	16	Q8FPI1	Q8fpi1 corynebacte
564	4	66.7	376	3	Q3UVU4	Q3UVU4 penicillium	637	4	66.7	423	8	Q05896	Q05896 beta vulgar
565	4	66.7	377	16	Q8PD85	Q8PD85 xanthomonas	638	4	66.7	423	10	Q9FH91	Q9fhn1 arabidopsis
566	4	66.7	379	16	Q8DLR0	Q8DLR0 synchococc	639	4	66.7	424	16	Q8ZAH6	Q8zah6 yersinia pe
567	4	66.7	380	16	Q8ZNL6	Q8ZNL6 salmonella	640	4	66.7	425	16	Q8XUM9	Q8xum9 ralatonia s
568	4	66.7	380	16	Q881J6	Q881J6 pseudomonas	641	4	66.7	426	12	Q8JL38	Q8j38 virus phich
569	4	66.7	380	16	Q8Z5A2	Q8Z5A2 salmonella	642	4	66.7	427	2	Q9RHZ6	Q9rh26 alicyclobac
570	4	66.7	381	16	Q83JR9	Q83JR9 rhizobium 1	643	4	66.7	428	16	Q7V028	Q7v028 prochloroco
571	4	66.7	381	16	Q9HY78	Q9HY78 pseudomonas	644	4	66.7	429	4	Q9HV78	Q9hv78 homo sapien
572	4	66.7	383	16	Q82GR3	Q82GR3 streptomyc	645	4	66.7	429	5	Q95Y50	Q95y50 caenorhabdi
573	4	66.7	384	12	Q9E6R3	Q9E6R3 turkey herp	646	4	66.7	429	16	Q50004	Q50004 mycobacteri
574	4	66.7	384	16	Q8PCC5	Q8PCC5 xanthomonas	647	4	66.7	429	16	Q7VA54	Q7va54 prochloroco
575	4	66.7	384	16	Q82ME1	Q82ME1 streptomyc	648	4	66.7	429	16	Q7TUN0	Q7tun0 prochloroco
576	4	66.7	385	5	Q9B1H6	Q9B1H6 anopheles g	649	4	66.7	430	16	Q9ADH5	Q9adh5 streptomyc
577	4	66.7	387	16	Q8XR48	Q8XR48 ralatonia s	650	4	66.7	430	16	Q8CW12	Q8cw12 yersinia pe
578	4	66.7	387	16	Q7WIA8	Q7WIA8 bordetella	651	4	66.7	430	16	Q8WDQ5	Q8wdq5 bordetella
579	4	66.7	387	16	Q7W6D9	Q7W6D9 bordetella	652	4	66.7	430	16	Q7W0J5	Q7w0j5 bordetella
580	4	66.7	388	10	Q9LUP8	Q9LUP8 arabidopsis	653	4	66.7	430	16	Q7V5R7	Q7v5r7 prochloroco
581	4	66.7	390	16	Q9ABM5	Q9ABM5 caulobacter	654	4	66.7	431	3	Q8NIP0	Q8nip0 cryptococcu
582	4	66.7	391	13	Q7T1J4	Q7T1J4 brachydanio	655	4	66.7	431	5	Q8SWI0	Q8swi0 encephalito
583	4	66.7	392	2	Q84H77	Q84H77 rhodococcus	656	4	66.7	431	10	Q84S41	Q84s41 oryza sativ
584	4	66.7	394	4	Q7Z593	Q7Z593 homo sapien	657	4	66.7	432	10	Q7XT41	Q7xt41 oryza sativ
585	4	66.7	395	2	Q9X412	Q9X412 chlamydia p	658	4	66.7	433	16	Q8G5Q6	Q8g5q6 bifidobacte
586	4	66.7	395	2	Q9S6B3	Q9S6B3 chlamydia p	659	4	66.7	434	16	Q82K42	Q82k42 streptomyc
587	4	66.7	395	16	Q8YGF2	Q8YGF2 bruceella me	660	4	66.7	436	16	Q81ZV9	Q81zv9 streptomyc
588	4	66.7	395	16	Q88KC3	Q88KC3 pseudomonas	661	4	66.7	437	2	Q7X410	Q7x410 pseudomonas
589	4	66.7	396	16	Q7WNA8	Q7WNA8 bordetella	662	4	66.7	438	16	Q8Y309	Q8y309 ralatonia s
590	4	66.7	396	16	Q7WBM4	Q7WBM4 bordetella	663	4	66.7	438	16	Q07183	Q07183 mycobacteri
591	4	66.7	397	16	Q8Q940	Q8Q940 bradyrhizob	664	4	66.7	438	16	Q7TY44	Q7ty44 mycobacteri
592	4	66.7	398	2	Q8KQ10	Q8KQ10 rhodococcus	665	4	66.7	439	2	Q84BF1	Q84bf1 xanthomonas
593	4	66.7	398	4	Q96KQ1	Q96KQ1 homo sapien	666	4	66.7	440	16	Q82LW1	Q82lw1 streptomyc
594	4	66.7	398	4	Q8WYN0	Q8WYN0 homo sapien	667	4	66.7	441	10	Q9S1I8	Q9s1i8 arabidopsis
595	4	66.7	398	12	Q9IBX1	Q9IBX1 turkey herp	668	4	66.7	443	16	Q9ZBI7	Q9zbi7 streptomyc
596	4	66.7	399	16	Q8ZOS1	Q8ZOS1 anabaena sp	669	4	66.7	445	16	Q9KPB7	Q9kpb7 vibrio chol
597	4	66.7	400	13	Q90YD6	Q90YD6 xenopus tro	670	4	66.7	448	16	Q88KW1	Q88kw1 pseudomonas
598	4	66.7	400	13	Q73818	Q73818 xenopus lae	671	4	66.7	449	16	Q06407	Q06407 mycobacteri
599	4	66.7	400	13	Q91703	Q91703 xenopus lae	672	4	66.7	449	16	Q7UI16	Q7uit6 mycobacteri
600	4	66.7	400	16	Q8YUD9	Q8YUD9 anabaena sp	673	4	66.7	450	5	Q8SXC2	Q8sxc2 drosophila

674	4	66.7	450	5	Q8T994	Q8t994 drosophila	747	4	66.7	477	16	Q92VB6	Q92ve6 rhizobium m
675	4	66.7	450	16	O33236	O33236 mycobacteri	748	4	66.7	477	16	Q7UW00	Q7uuw0 rhodopirell
676	4	66.7	450	16	Q9RJ91	Q9rj91 streptomyc	749	4	66.7	477	17	Q970V3	Q970v3 sulfolobus
677	4	66.7	450	16	Q7TY07	Q7ty07 mycobacteri	750	4	66.7	478	2	Q8GIE3	Q8gie3 mycoplasma
678	4	66.7	451	2	Q56758	Q56758 xanthobacte	751	4	66.7	478	2	Q8GIE0	Q8gie0 mycoplasma
679	4	66.7	451	16	Q7UMJ4	Q7umj4 rhodopirell	752	4	66.7	478	4	Q9H0J7	Q9h0j7 homo sapien
680	4	66.7	452	2	O66239	O66239 escherichia	753	4	66.7	478	10	Q7XJ05	Q7xj05 oryza sativ
681	4	66.7	452	2	O66235	O66235 escherichia	754	4	66.7	480	16	Q88588	Q88588 pseudomonas
682	4	66.7	452	2	O70051	O70051 klebsiella	755	4	66.7	480	16	Q7UY49	Q7uy49 rhodopirell
683	4	66.7	452	2	O70051	O70051 klebsiella	756	4	66.7	481	16	Q8DI14	Q8di14 synecococc
684	4	66.7	452	5	O61918	O61918 caenorhabdi	757	4	66.7	482	16	Q82CN7	Q82cn7 streptomyc
685	4	66.7	452	16	Q8ZL19	Q8z119 salmonella	758	4	66.7	482	16	Q82CP3	Q82cp3 streptomyc
686	4	66.7	452	16	Q82ZK1	Q82z19 nitrosomona	759	4	66.7	482	16	Q82CP3	Q82cp3 streptomyc
687	4	66.7	452	16	Q82VS7	Q82vs7 bacillus an	760	4	66.7	483	17	Q9UX28	Q9ux28 sulfolobus
688	4	66.7	452	16	Q81R45	Q81r45 bacillus ha	761	4	66.7	484	5	Q9XU48	Q9xua8 caenorhabdi
689	4	66.7	453	5	Q9Z9T3	Q9z9t3 bacillus ha	762	4	66.7	484	16	Q8XDJ5	Q8xdj5 escherichia
690	4	66.7	453	5	Q9VZ57	Q9vz57 drosophila	763	4	66.7	484	16	Q8XDU5	Q8xdu5 escherichia
691	4	66.7	453	12	Q67215	Q67215 influenzavi	764	4	66.7	484	16	Q83I19	Q83i19 shigella fl
692	4	66.7	453	12	Q67217	Q67217 influenzavi	765	4	66.7	486	13	Q804D8	Q804d8 bufo arenar
693	4	66.7	453	12	Q67216	Q67216 influenzavi	766	4	66.7	487	10	Q7XV19	Q7xv19 oryza sativ
694	4	66.7	453	16	Q8KG44	Q8kg44 chlorobium	767	4	66.7	487	16	Q8DB92	Q8db92 vibrio vuln
695	4	66.7	454	2	Q9RMU5	Q9rmu5 klebsiella	768	4	66.7	489	5	Q8IRK2	Q8irk2 drosophila
696	4	66.7	454	10	Q40100	Q40100 ipomoea tri	769	4	66.7	489	16	P96223	P96223 mycobacteri
697	4	66.7	454	12	Q8JU04	Q8juu4 influenza a	770	4	66.7	489	16	P96223	P96223 mycobacteri
698	4	66.7	454	12	Q8JU04	Q8juu4 influenza a	771	4	66.7	489	16	Q7TV12	Q7tv12 mycobacteri
699	4	66.7	457	10	Q84KH1	Q84kh1 triticum mo	772	4	66.7	491	4	Q9H8X2	Q9h8x2 homo sapien
700	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	773	4	66.7	491	4	Q9H8X2	Q9h8x2 homo sapien
701	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	774	4	66.7	491	16	Q91218	Q91218 pseudomonas
702	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	775	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
703	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	776	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
704	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	777	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
705	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	778	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
706	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	779	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
707	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	780	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
708	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	781	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
709	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	782	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
710	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	783	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
711	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	784	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
712	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	785	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
713	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	786	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
714	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	787	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
715	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	788	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
716	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	789	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
717	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	790	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
718	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	791	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
719	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	792	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
720	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	793	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
721	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	794	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
722	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	795	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
723	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	796	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
724	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	797	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
725	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	798	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
726	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	799	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
727	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	800	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
728	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	801	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
729	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	802	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
730	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	803	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
731	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	804	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
732	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	805	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
733	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	806	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
734	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	807	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
735	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	808	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
736	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	809	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
737	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	810	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
738	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	811	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
739	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	812	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
740	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	813	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
741	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	814	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
742	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	815	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
743	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	816	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
744	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	817	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
745	4	66.7	457	16	Q8GSA0	Q8gsa0 bifidobacte	818	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila
746	4	66.7	457	16	Q8UHM4	Q8uhm4 agrobacteri	819	4	66.7	492	5	Q9W1H3	Q9w1h3 drosophila

820	4	66.7	534	17	Q8PSW2	Q8psw2 methanosarc	893	4	66.7	606	13	Q91916	Q91916 brachydanio
821	4	66.7	535	16	Q8G5P4	Q8g5p4 bifidobacte	894	4	66.7	606	13	Q7ZU27	Q7zu27 brachydanio
822	4	66.7	536	16	Q05459	Q05459 mycobacteri	895	4	66.7	606	16	Q8FB08	Q8fb08 escherichia
823	4	66.7	537	16	Q7TVF5	Q7tvf5 mycobacteri	896	4	66.7	606	16	Q82KE7	Q82ke7 streptomyce
824	4	66.7	538	11	Q8C9K6	Q8c9k6 mus musculu	897	4	66.7	607	10	Q91LGJ7	Q91lgj7 oryza sativ
825	4	66.7	539	5	Q77059	Q77059 mus musculu	898	4	66.7	608	12	Q80MY5	Q80my5 human cytom
826	4	66.7	540	5	Q9TVAO	Q9tva0 drosophila	899	4	66.7	608	12	Q80MY1	Q80my1 human cytom
827	4	66.7	541	5	Q8KBZ8	Q8kbz8 chlorobium	900	4	66.7	609	5	Q9SX10	Q9sx10 drosophila
828	4	66.7	542	16	Q8KN49	Q8kn49 sphingobium	901	4	66.7	609	11	Q8K4B2	Q8k4b2 mus musculu
829	4	66.7	543	5	Q27659	Q27659 giardia lam	902	4	66.7	609	11	Q8C7U8	Q8c7u8 mus musculu
830	4	66.7	544	5	Q8KN49	Q8kn49 sphingobium	903	4	66.7	609	11	Q8C7U8	Q8c7u8 mus musculu
831	4	66.7	545	12	Q8P9475	Q8p9475 herpes simp	904	4	66.7	609	17	Q8CE40	Q8ce40 mus musculu
832	4	66.7	546	16	Q8U615	Q8u615 agrobacteri	905	4	66.7	609	17	Q97WE1	Q97we1 sulfolobus
833	4	66.7	547	2	Q93317	Q93317 chlamydia t	906	4	66.7	611	10	Q84TA3	Q84ta3 oryza sativ
834	4	66.7	547	10	Q8H1F0	Q8h1f0 arabidopsis	907	4	66.7	612	8	Q8HMF9	Q8hmf9 sirmo imb
835	4	66.7	547	10	Q8SAM6	Q8sam6 oryza sativ	908	4	66.7	612	8	Q8HMF9	Q8hmf9 sirmo imb
836	4	66.7	547	10	Q8RXK4	Q8rxk4 arabidopsis	909	4	66.7	613	16	Q8HMF9	Q8hmf9 sirmo imb
837	4	66.7	547	10	Q7XGL6	Q7xgl6 oryza sativ	910	4	66.7	613	16	Q8HMF9	Q8hmf9 sirmo imb
838	4	66.7	547	16	Q9RZJ4	Q9rzj4 deinococcus	911	4	66.7	616	13	Q80MY1	Q80my1 human cytom
839	4	66.7	548	17	Q9HPQ3	Q9hpq3 halobacteri	912	4	66.7	617	16	Q81YD8	Q81yd8 bacillus lae
840	4	66.7	550	3	Q9C124	Q9c124 pichia past	913	4	66.7	617	16	Q81YD8	Q81yd8 bacillus lae
841	4	66.7	550	5	Q9NGI8	Q9ngi8 trypanosoma	914	4	66.7	620	16	Q8FZX3	Q8fzx3 brucella au
842	4	66.7	553	5	Q8GN96	Q8gn96 leishmania	915	4	66.7	621	13	Q8G611	Q8g611 gallus gall
843	4	66.7	553	10	Q9T0J7	Q9t0j7 arabidopsis	916	4	66.7	621	13	Q8G611	Q8g611 gallus gall
844	4	66.7	553	16	Q8XWP8	Q8xwp8 raietonia s	917	4	66.7	621	16	Q7UT91	Q7ut91 rhodopirell
845	4	66.7	553	16	Q8C2P9	Q8c2p9 yersinia pe	918	4	66.7	623	5	Q9V534	Q9v534 drosophila
846	4	66.7	554	16	Q9PJVO	Q9pjvo chlamydia m	919	4	66.7	626	4	Q8N491	Q8n491 homo sapien
847	4	66.7	556	10	Q94CQ2	Q94cq2 oryza sativ	920	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
848	4	66.7	556	13	Q91917	Q91917 brachydanio	921	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
849	4	66.7	556	16	Q34650	Q34650 bacillus au	922	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
850	4	66.7	557	2	Q9ATS7	Q9ais7 chlamydomo	923	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
851	4	66.7	557	10	Q94KV1	Q94kv1 chlamydomo	924	4	66.7	627	10	Q9MAS7	Q9mas7 arabidopsis
852	4	66.7	557	16	Q8A5P5	Q8a5p5 bacteroides	925	4	66.7	628	5	Q9V534	Q9v534 drosophila
853	4	66.7	557	16	Q834P1	Q834p1 enterococcu	926	4	66.7	628	5	Q9V534	Q9v534 drosophila
854	4	66.7	558	2	Q9R9W8	Q9r9w8 pseudomonas	927	4	66.7	628	5	Q9V534	Q9v534 drosophila
855	4	66.7	559	16	Q8PQT4	Q8pqt4 xanthomonas	928	4	66.7	628	5	Q9V534	Q9v534 drosophila
856	4	66.7	560	11	Q81LL3	Q81ll3 mus musculu	929	4	66.7	628	5	Q9V534	Q9v534 drosophila
857	4	66.7	567	16	Q8XED6	Q8xed6 escherichia	930	4	66.7	628	5	Q9V534	Q9v534 drosophila
858	4	66.7	567	16	Q8ZDN4	Q8zdn4 yersinia pe	931	4	66.7	628	5	Q9V534	Q9v534 drosophila
859	4	66.7	570	5	Q9GRS7	Q9grs7 leishmania	932	4	66.7	628	5	Q9V534	Q9v534 drosophila
860	4	66.7	571	11	Q8CG36	Q8cg36 mus musculu	933	4	66.7	628	5	Q9V534	Q9v534 drosophila
861	4	66.7	572	5	Q9GSR0	Q9gsr0 plasmodium	934	4	66.7	628	5	Q9V534	Q9v534 drosophila
862	4	66.7	576	2	Q87870	Q87870 thauera aro	935	4	66.7	628	5	Q9V534	Q9v534 drosophila
863	4	66.7	576	2	Q7WSH6	Q7wsh6 comamonas t	936	4	66.7	628	5	Q9V534	Q9v534 drosophila
864	4	66.7	577	4	Q81YH3	Q81yh3 homo sapien	937	4	66.7	628	5	Q9V534	Q9v534 drosophila
865	4	66.7	577	10	Q9ATG6	Q9atg6 polytomella	938	4	66.7	628	5	Q9V534	Q9v534 drosophila
866	4	66.7	578	4	Q9NS49	Q9ns49 homo sapien	939	4	66.7	628	5	Q9V534	Q9v534 drosophila
867	4	66.7	579	16	Q987P1	Q987f1 rhizobium l	940	4	66.7	628	5	Q9V534	Q9v534 drosophila
868	4	66.7	583	11	Q8CH93	Q8ch93 rattus norv	941	4	66.7	628	5	Q9V534	Q9v534 drosophila
869	4	66.7	584	5	Q8MKT8	Q8mkt8 drosophila	942	4	66.7	628	5	Q9V534	Q9v534 drosophila
870	4	66.7	584	16	Q98NT7	Q98nt7 rhizobium l	943	4	66.7	628	5	Q9V534	Q9v534 drosophila
871	4	66.7	584	17	Q8TQM7	Q8tqm7 methanosarc	944	4	66.7	628	5	Q9V534	Q9v534 drosophila
872	4	66.7	586	4	Q16526	Q16526 homo sapien	945	4	66.7	628	5	Q9V534	Q9v534 drosophila
873	4	66.7	586	6	Q8WPI9	Q8wpi9 macaca fasc	946	4	66.7	628	5	Q9V534	Q9v534 drosophila
874	4	66.7	587	16	Q8ZG34	Q8zg34 yersinia pe	947	4	66.7	628	5	Q9V534	Q9v534 drosophila
875	4	66.7	587	16	Q7UF83	Q7ufe83 rhodopirell	948	4	66.7	628	5	Q9V534	Q9v534 drosophila
876	4	66.7	588	12	Q82G94	Q82g94 streptomyce	949	4	66.7	628	5	Q9V534	Q9v534 drosophila
877	4	66.7	588	16	Q9Q1V2	Q9q1v2 rabbit pico	950	4	66.7	628	5	Q9V534	Q9v534 drosophila
878	4	66.7	590	16	Q89VN6	Q89vn6 bradyrhizob	951	4	66.7	628	5	Q9V534	Q9v534 drosophila
879	4	66.7	591	16	Q8A2L3	Q8a2l3 bacteroides	952	4	66.7	628	5	Q9V534	Q9v534 drosophila
880	4	66.7	593	2	Q8L1B4	Q8l1e4 synechococc	953	4	66.7	628	5	Q9V534	Q9v534 drosophila
881	4	66.7	594	13	Q803K2	Q803k2 brachydanio	954	4	66.7	628	5	Q9V534	Q9v534 drosophila
882	4	66.7	596	4	Q9Y616	Q9y616 homo sapien	955	4	66.7	628	5	Q9V534	Q9v534 drosophila
883	4	66.7	598	13	Q91913	Q91913 brachydanio	956	4	66.7	628	5	Q9V534	Q9v534 drosophila
884	4	66.7	598	13	Q72U53	Q7zu53 brachydanio	957	4	66.7	628	5	Q9V534	Q9v534 drosophila
885	4	66.7	599	16	Q8YHY8	Q8yhy8 brucella me	958	4	66.7	628	5	Q9V534	Q9v534 drosophila
886	4	66.7	600	2	Q66396	Q66396 acinetobact	959	4	66.7	628	5	Q9V534	Q9v534 drosophila
887	4	66.7	601	16	Q8F864	Q8f864 leptospira	960	4	66.7	628	5	Q9V534	Q9v534 drosophila
888	4	66.7	602	16	Q8YYP3	Q8yyp3 anabaena sp	961	4	66.7	628	5	Q9V534	Q9v534 drosophila
889	4	66.7	602	16	Q9S218	Q9s218 streptomyce	962	4	66.7	628	5	Q9V534	Q9v534 drosophila
890	4	66.7	602	16	Q8F426	Q8f426 leptospira	963	4	66.7	628	5	Q9V534	Q9v534 drosophila
891	4	66.7	602	16	Q82J57	Q82j57 streptomyce	964	4	66.7	628	5	Q9V534	Q9v534 drosophila
892	4	66.7	606	11	P97784	P97784 mus musculu	965	4	66.7	628	5	Q9V534	Q9v534 drosophila

966 4 66.7 679 16 Q8ZD61 Q8zd61 yersinia pe
 967 4 66.7 680 8 Q9SGC6 Q9sgc6 panicum obt
 968 4 66.7 680 10 Q9SY66 Q9sy66 arabidopsis
 969 4 66.7 682 8 Q9SG6 Q9sg6 paspalum co
 970 4 66.7 683 8 Q9SGB5 Q9sgb5 paspalum we
 971 4 66.7 683 8 Q9SGB7 Q9sgb7 paspalum re
 972 4 66.7 683 8 Q9SGCO Q9sgco paspalum va
 973 4 66.7 683 8 Q9SGC1 Q9sgc1 paspalum ha
 974 4 66.7 683 8 Q9SGB8 Q9sgb8 paspalum pa
 975 4 66.7 683 8 Q9SG95 Q9sg95 thraasya pet
 976 4 66.7 683 8 Q9SGB9 Q9sgb9 paspalum co
 977 4 66.7 683 8 Q9SGB4 Q9sgb4 paspalum ma
 978 4 66.7 683 16 Q9PD83 Q9pd83 xylella fas
 979 4 66.7 683 16 Q87DH4 Q87dh4 xylella fas
 980 4 66.7 687 2 Q9L807 Q9l807 pseudomonas
 981 4 66.7 688 8 Q9SGG5 Q9sgg5 anthaenanti
 982 4 66.7 689 8 Q9SX6 Q9sx6 panicum tue
 983 4 66.7 690 8 Q9SG96 Q9sg96 thraasya gla
 984 4 66.7 691 8 Q9SGC2 Q9sgc2 paspalum ar
 985 4 66.7 695 2 Q8KXD6 Q8kxd6 actinobacil
 986 4 66.7 699 16 Q8ZCD5 Q8zcd5 yersinia pe
 987 4 66.7 699 16 Q8CLD1 Q8clld1 yersinia pe
 988 4 66.7 699 17 Q8THR8 Q8thr8 methanosarc
 989 4 66.7 700 8 P92298 P92298 gmelina hys
 990 4 66.7 702 16 Q8A315 Q8a315 bacteroides
 991 4 66.7 703 10 Q9FHJ0 Q9fhj0 arabidopsis
 992 4 66.7 703 10 Q9FIS0 Q9fis0 arabidopsis
 993 4 66.7 703 10 Q8GVG3 Q8gvg3 arabidopsis
 994 4 66.7 703 16 Q8XTK8 Q8xtk8 ralstonia s
 995 4 66.7 706 2 Q8KT79 Q8kt79 gamma-prote
 996 4 66.7 706 16 Q7UQT4 Q7uqt4 rhodospirell
 997 4 66.7 707 8 Q9MVH4 Q9mvh4 colona scab
 998 4 66.7 707 16 P73608 P73608 symeochocyst
 999 4 66.7 708 4 Q7Z2K9 Q7z2k9 homo sapien
 1000 4 66.7 711 8 Q9MVG7 Q9mvg7 grewia bilo

ALIGNMENTS

RESULT 1

Q9ACRS PRELIMINARY; PRT; 205 AA.
 AC Q9ACRS5;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Hypothetical protein SCPl.253.
 GN SCPl.253.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=21996410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL; AL590464; CAC36779.1; --
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Hypothetical protein; Plasmid; Complete proteome.

SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;
 Query Match 83.3%; Score 5; DB 16; Length 205;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 Db 10 ADMSW 14
 RESULT 2
 Q81XK8 PRELIMINARY; PRT; 227 AA.
 ID Q81XK8;
 AC Q81XK8; (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Similar to hypothetical protein BC017335.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC040173; AAH40173.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 227 AA; 25487 MW; F11A71EA57062A05 CRC64;
 Query Match 83.3%; Score 5; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADMSW 5
 Db 113 ADMSW 117
 RESULT 3
 Q7YCU8 PRELIMINARY; PRT; 228 AA.
 ID Q7YCU8;
 AC Q7YCU8; (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Cytochrome oxidase subunit II.
 OS Sphenodon punctatus (Hatteria) (Tuatara).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
 OX NCBI_TaxID=8508;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rest J.S., Aet J.C., Austin C.C., Waddell P.J., Tibbetts E.A.,
 RA Hay J.M., Mindell D.P.;
 RT "Molecular systematics of primary reptilian lineages and the tuatara
 Mol. Phylogenetic Evol. 0:0-0(2003).
 RL EMBL; AF534390; AAP42708.1; --
 KW Mitochondrion.
 SQ SEQUENCE 228 AA; 25903 MW; AC52448F76C9F0A4 CRC64;
 Query Match 83.3%; Score 5; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DMSWA 6
 Db 221 DMSWA 225

RESULT 4

Q8NJY9 PRELIMINARY; PRT; 236 AA.
 AC Q8NJY9;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Endoglucanase.
 GN CEL12C.
 OS Bionectria ochroleuca (Gliocladium roseum).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.
 OX NCBI_TaxID=29856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22067395; PubMed=12073090;
 RA Goedegebuur F., Fowler T., Phillips J., van der Kley P.,
 RA van Solingen P., Dankmeyer L., Power S.D.;
 RT "Cloning and relational analysis of 15 novel fungal endoglucanases
 from family 12 glycosyl hydrolase.";
 RL Curr. Genet. 41:89-98(2002).
 DR EMBL; AF435065; AAM77708.1; -;
 DR GO; GO:000810; P:cellulase activity; IEA.
 DR GO; GO:0000272; P:polysaccharide catabolism; IEA.
 DR InterPro; IPR008985; ConA-like_lccgl.
 DR InterPro; IPR002594; Glyco_hydro_12.
 DR Pfam; PF01670; Glyco_hydro_12; 1.
 DR ProDom; PD004316; Glyco_hydro_12; 1.
 SQ SEQUENCE 236 AA; 26024 MW; C3D8A7E33F0C41D8 CRC64;

Query Match 83.3%; Score 5; DB 3; Length 236;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

Db 63 ADMSW 67
 |||||

RESULT 5

Q919K8 PRELIMINARY; PRT; 242 AA.
 AC Q919K8;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE CUN068 hypothetical protein.
 GN CUN068.
 OS Culex nigripalpus baculovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
 OX NCBI_TaxID=130556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Florida1997;
 RX MEDLINE=21488685; PubMed=11602755;
 RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.;
 RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";
 RL J. Virol. 75:11157-11165(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Florida1997;
 RA Alfonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,
 RA Becnel J.J., Rock D.L., Kutish G.F.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF403738; AAK94146.1; -;
 KW Hypothetical protein.
 SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 83.3%; Score 5; DB 12; Length 242;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

Db 2 DMSWA 6
 |||||
 Db 80 DMSWA 84

RESULT 6

Q8G659 PRELIMINARY; PRT; 274 AA.
 ID Q8G659
 AC Q8G659;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Probable dihydroototate dehydrogenase electron transfer subunit.
 GN PRK OR EL0790.
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 OC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Schell M.A., Karmirantzou M., Snel B., Villanova D., Berger B.,
 RA Pessi G., Zwielen M.-C., Desiere F., Bork P., Delley M.,
 RA Pidmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 to the human gastrointestinal tract.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 DR EMBL; AE014701; AAN24605.1; -;
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR008333; FAD_binding_6.
 DR Pfam; PF00970; FAD_binding_6; 1.
 KW Complete proteome.
 SQ SEQUENCE 274 AA; 29978 MW; 971E0016E79636DB CRC64;

Query Match 83.3%; Score 5; DB 16; Length 274;
 Best Local Similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5

Db 171 ADMSW 175
 |||||

RESULT 7

Q8BIT9 PRELIMINARY; PRT; 355 AA.
 ID Q8BIT9
 AC Q8BIT9;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Mitochondrial ribosomal protein L41 homolog.
 GN 2810443J12RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK087998; BAC40084.1; -;
 DR MGD; MGI:1914478; 2810443J12RIK.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 2.
 DR SMART; SM00320; WD40; 4.

```
DR PROSITE; PS00678; WD REPEATS 1; 1.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
SQ SEQUENCE 355 AA; 40183 MW; FEF8546127402D58 CRC64;

Query Match      83.3%; Score 5; DB 11; Length 355;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADMSW 5
Db      215 ADMSW 219
      |||||

RESULT 8
O50002      PRELIMINARY;      PRT;      358 AA.
AC O50002;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=36596;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bergeron; TISSUE=Mesocarp, and Exocarp;
RA Mbeguite-A-Mbeguite D., Gomez R.-M., Fills-Lycaon B.;
RT "Sequence of APTP1, a Cysteine Proteinase From Apricot Fruit
  (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
  179).";
RL Plant Physiol. 115:1730-1730 (1997).
DR EMBL; U93166; AAB97142.1; -.
DR HSSP; P07711; 1CUL.
DR MEROPS; C01.041; -.
DR GO; GO:0004197; P: cysteine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR001092; HLH basic.
DR InterPro; IPR000668; Peptidase_C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase_C1; 1.
DR PRINTS; PR00705; PAPAIN.
DR ProDom; PD000158; Peptidase_C1; 1.
DR SMART; SM00645; Pept_C1; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; 1.
DR PROSITE; PS00139; THIOL_PROTEASE CYS; 1.
DR PROSITE; PS00639; THIOL_PROTEASE HIS; 1.
DR Hydrolase; Protease; Thiol protease.
KW SEQUENCE 358 AA; 39309 MW; C98F78793B002554 CRC64;

Query Match      83.3%; Score 5; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADMSW 5
Db      108 ADMSW 112
      |||||

RESULT 9
Q9HZ10      PRELIMINARY;      PRT;      374 AA.
AC Q9HZ10;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
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OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
  opportunistic pathogen.";
RL Nature 406:959-964 (2000).
DR EMBL; AE004746; AAG06618.1; -.
DR FIR; B83241; B83241.
DR InterPro; IPR007434; DUF482.
DR Pfam; PF04339; DUF482; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MW; 31EF185C4F683884 CRC64;

Query Match      83.3%; Score 5; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      81 DWSWA 85
      |||||

RESULT 10
Q86KSO      PRELIMINARY;      PRT;      375 AA.
AC Q86KSO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RX MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RL Nature 418:79-85 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC115612; AA050929.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0008152; P: metabolism; IEA.
DR InterPro; IPR000581; ILVD_EDD_family.
DR InterPro; IPR006970; PT.
DR Pfam; PF04886; PT; 1.
DR PROSITE; PS00886; ILVD_EDD_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 375 AA; 41862 MW; EC9A1D744C56856E CRC64;

Query Match      83.3%; Score 5; DB 5; Length 375;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      47 DWSWA 51
      |||||
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RESULT 11
Q86KF9 PRELIMINARY; PRT; 426 AA.
AC Q86KF9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Similar to Mus musculus (Mouse). DnaJ homolog subfamily B member 5
DE (Heat shock protein Hsp40-3) (Heat shock protein cognate 40)
DE (Hsc40).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RC MEDLINE=22092622; PubMed=12097910;
RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
RA "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
RA Nature 418:79-85(2002).
RL Nature 418:79-85(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
RA Baumgart C.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC115680; AA051091.1; -
DR GO: GO:0003773; P:heat shock protein activity; IEA.
DR InterPro: IPR001623; DnaJ_N.
DR Pfam: PF00226; DnaJ_1.
DR PRINTS: SM00271; DnaJ_1.
DR PROSITE: PS00636; DnaJ_1; 1.
DR PROSITE: PS00636; DnaJ_2; 1.
KW Heat shock.
SQ SEQUENCE 426 AA; 48376 MW; EBF9F37295925727 CRC64;

Query Match 83.3%; Score 5; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 127 DWSWA 131

RESULT 12
Q8P4A1 PRELIMINARY; PRT; 433 AA.
AC Q8P4A1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Cationic amino acid transporter.
GN XCC3809.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RC MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RA host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AB012036; AA038706.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.

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RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RA host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AB012502; AA043483.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.
DR Pfam: PF00324; aa_permease; I.
KW Complete proteome.
SQ SEQUENCE 433 AA; 45128 MW; EBF21D2A7C516533 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 433;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 181 DWSWA 185

RESULT 13
Q8PFV8 PRELIMINARY; PRT; 438 AA.
AC Q8PFV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cationic amino acid transporter.
GN XAC3864.
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RC MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RA host specificities.";
RL Nature 417:459-463(2002).
DR EMBL: AB012036; AA038706.1; -
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO: GO:0006865; P:amino acid transport; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR002293; AA/rel_permease1.

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DR InterPro: IPR004841; Permease region.
DR Pfam: PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 438 AA; 45795 MW; 921AC5AC60A545E2 CRC64;

Query Match      83.3%; Score 5; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 183 DMSWA 187

RESULT 14
Q96AB7 PRELIMINARY; PRT; 452 AA.
AC Q96AB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90634.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Skin;
RC Strausberg R.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RA Isoai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC017335; AAH17335.1; -.
DR ENBL; AK075115; BAC11411.1; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 2.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MW; B79D25BE38096733 CRC64;

Query Match      83.3%; Score 5; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 338 ADMSW 342

RESULT 15
Q8MWJ0 PRELIMINARY; PRT; 463 AA.
AC Q8MWJ0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Major royal jelly protein MRJP2 precursor.
GN MRJP2.
OS Apis cerana (Indian honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.

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OX NCBI_TaxID=7461;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Nurse heads;
RA "Moleculare S.; Imjongjirak C.;
RT "Molecular Cloning of Major Royal Jelly Protein (MRJP2) cDNA from Apis
RT cerana in Thailand.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; AF525777; AAM88282.1; -.
DR InterPro: IPR003534; Royaljelly.
DR Pfam: PF03022; MRJP; 1.
DR PRINTS; PR01366; ROYALJELLY.
KW Signal.
FT SIGNAL 1 17 POTENTIAL.
SQ SEQUENCE 463 AA; 52412 MW; D648AE2BAF1EDDE9 CRC64;

Query Match      83.3%; Score 5; DB 5; Length 463;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSWA 6
Db 110 DMSWA 114

RESULT 16
Q7TF27 PRELIMINARY; PRT; 470 AA.
AC Q7TF27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neuraminidase.
OS Influenza A virus (A/duck/NY/191255-59/02(H5N8)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=232442;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=A/duck/NY/191255-59/02;
RA Lee C.-W., Senne D., Linares J.A., Woolcock P., Stallnecht D.,
RA Spackman E., Swane D., Suarez D.;
RT "Characterization of recent H5 subtype avian influenza viruses from
RT U.S. poultry.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY300948; AAP57560.1; -.
SQ SEQUENCE 470 AA; 52260 MW; 41470434D8ED1662 CRC64;

Query Match      83.3%; Score 5; DB 12; Length 470;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
Db 453 ADMSW 457

RESULT 17
Q9CYU6 PRELIMINARY; PRT; 477 AA.
AC Q9CYU6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 2810443J12Rik protein (Mitochondrial ribosomal protein L41
DE homolog).
GN 2810443J12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.

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RC STRAIN=CS7BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Mesonephros;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK013297; BAB28775.1; -.
DR MGD; MGI:1914478; BAC37279.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 477 AA; 53201 MW; 2555573524A4BA9C CRC64;

Query Match 83.3%; Score 5; DB 11; Length 477;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 337 ADMSW 341
|||||

RESULT 18
Q9BT6
ID Q9BT6 - PRELIMINARY; PRT; 484 AA.
AC Q9BT6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Strauberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003123; AA03123.1; -.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 3.

DR PROSITE; PS00678; WD_REPEATS_1; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
FT NON TER 1
SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7359E CRC64;

Query Match 83.3%; Score 5; DB 4; Length 484;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 370 ADMSW 374
|||||

RESULT 19
Q8MSH3
ID Q8MSH3 PRELIMINARY; PRT; 581 AA.
AC Q8MSH3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GH24640P.
GN NINAG OR CG5728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Calniker S.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV118818; AAM50678.1; -.
DR FlyBase; FBgn0037896; ninag.
DR GO; GO:0004197; F:cysteine-type endopeptidase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000172; GMC Oxred.
DR InterPro; IPR007867; GMC Oxred_C.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF05199; GMC Oxred_C; 1.
DR Pfam; PF00732; GMC Oxred_N; 1.
DR PROSITE; PS00639; THIOI PROTEASE HIS; 1.
SQ SEQUENCE 581 AA; 63475 MW; A2F13BEC25E496D CRC64;

Query Match 83.3%; Score 5; DB 5; Length 581;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 159 DWSWA 163
|||||

RESULT 20
Q9VGP2
ID Q9VGP2 PRELIMINARY; PRT; 597 AA.
AC Q9VGP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG6728 protein.
GN NINAG OR CG5728.
OS Drosophila melanogaster (Fruit fly).

AC Q82MX2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative nitric oxide synthase.
GN SAV1531.
OS Streptomyces avermitilis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCB TaxID=33903;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=11572948;
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.,
RT "Genome sequence of an industrial microorganism Streptomyces
RT avermitilis; deducing the ability of producing secondary
RT metabolites.";
RN Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX MEDLINE=21477403; PubMed=12692562;
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA Sakaki Y., Hattori M., Omura S.,
RT "Complete genome sequence and comparative analysis of the industrial
RT microorganism Streptomyces avermitilis.";
RL Nat. Biotechnol. 21:526-531(2003).
DR EMBL; AF005027; BAC69241.1;
DR GO; GO:0004517; F: nitric oxide synthase activity; IEA.
DR GO; GO:0006809; P: nitric oxide biosynthesis; IEA.
DR InterPro; IPR004030; NO synthase.
DR Pfam; PF02898; NO synthase; 1.
DR PROSITE; PS60001; NOS; 1.
RW Complete proteome.
SQ SEQUENCE 605 AA; 65534 MW; 8208F93B381C1FF5 CRC64;
Query Match 83.3%; Score 5; DB 16; Length 605;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 556 ADWSW 560
RESULT 22
Q9AAZ6 PRELIMINARY; PRT; 889 AA.
AC Q9AAZ6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE TonB-dependent receptor.
GN CC0446.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCB TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri J., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCB TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berner B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milchina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
EMBL; AF003691; AAF54634.1; ..
DR FlyBase; FBgn0037896; ninaG.
DR GO; GO:0004197; F: cytochrome-type endopeptidase activity; IEA.
DR GO; GO:0016491; F: oxidoreductase activity; IEA.
DR GO; GO:0006118; P: electron transport; IEA.
DR GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro; IPR000172; GMC_oxred.
DR InterPro; IPR007867; GMC_oxred.
DR InterPro; IPR00169; SHprot_acsite.
DR Pfam; PF05199; GMC_oxred C; 1.
DR Pfam; PF00732; GMC_oxred N; 1.
DR PROSITE; PS00624; GMC_oxred 2; 1.
DR PROSITE; PS00639; THIOL PROTEASE HIS; 1.
SQ SEQUENCE 597 AA; 65274 MW; 82C362AFA0902A CRC64;
Query Match 83.3%; Score 5; DB 5; Length 597;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSWA 6
Db 159 DWSWA 163
RESULT 21
Q82MX2 PRELIMINARY; PRT; 605 AA.
ID Q82MX2

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005717; AAK22433.1; -.
DR PIR; E87304; E87304.
DR TIGR; CC0446; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; F:transport; IEA.
DR InterPro; IPR000531; TonB_boxC.
DR Pfam; PF00593; TonB_dep_Rec; 1.
DR KW Receptor; Complete proteome.
SQ SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;

Query Match 83.3%; Score 5; DB 16; Length 889;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
| | | | |
DB 618 ADMSW 622

RESULT 23

Q9XGZ2 PRELIMINARY; PRT; 1005 AA.
ID Q9XGZ2 PRELIMINARY; PRT; 1005 AA.
AC Q9XGZ2; PRELIMINARY; PRT; 1005 AA.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T1N24.22 protein (Putative receptor protein kinase).
DE T1N24.22 OR A15G25930.
GN Arabidopsis thaliana (Mouse-ear cress).
OS Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA WashU;
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Murray J., Langston Y., Clarke K., Drone K.;
RT "The sequence of A. thaliana T1N24.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Waterston R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF149413; AAD40144.1; -.
DR EMBL; BT004058; AAO42089.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001611; LRR.

DR InterPro; IPR007090; LRR_plant.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00560; LRR; 8.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICHRPT.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferase;
SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

Query Match 83.3%; Score 5; DB 10; Length 1005;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
| | | | |
DB 906 ADMSW 910

RESULT 24

Q9L4X2 PRELIMINARY; PRT; 5435 AA.
ID Q9L4X2 PRELIMINARY; PRT; 5435 AA.
AC Q9L4X2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NYSJ.
GN Streptomyces noursei.
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1971;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 11455;
RX MEDLINE=20334850; PubMed=10873841;
RA Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,
RA Valla S., Zotchev S.B.;
RT "Biosyntheses of the polyene antifungal antibiotic nystatin in
RT Streptomyces noursei ATCC 11455: analysis of the gene cluster and
RT deduction of the biosynthetic pathway.";
RL Chem. Biol. 7:395-403(2000).
CC -1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY; AAF71767.1; -.
DR EMBL; AF263912; AAF71767.1; -.
DR HSSP; P25715; IMLA.
DR GO; GO:0004024; F:alcohol dehydrogenase activity; zinc-dependent; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0004314; F:[acyl-carrier protein] S-malonyltransferase. . .; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001227; Ac trans.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR02085; Adh_zn_family.
DR InterPro; IPR004410; Fabb.
DR InterPro; IPR00794; Ketoacyl_synth.
DR InterPro; IPR006162; Ppantne S.
DR InterPro; IPR006163; Pp_bind.
DR Pfam; PF00698; Acyl_transf; 3.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF00107; ADH_zinc_N; 1.
DR Pfam; PF00109; ketoacyl-synt; 3.
DR Pfam; PF02801; ketoacyl-synt C; 3.
DR Pfam; PF00550; pp-binding; 3.
DR TIGRfams; TIGR00128; fabb; 3.
DR PROSITE; PS00075; ACP_DOMAIN; 3.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 3.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 3.
KW Oxidoreductase; Phosphopantetheine; Transferase.
SQ SEQUENCE 5435 AA; 562659 MW; AA55465DF087A38C CRC64;

Query Match 83.3%; Score 5; DB 2; Length 5435;
Best Local Similarity 100.0%; Pred. No. 8.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0

QY 1 ADWSW 5
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DB 1525 ADWSW 1529

RESULT 25
Q46496 PRELIMINARY; PRT; 53 AA.

ID Q46496 AC Q46496; (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Rubredoxin.
GN RUB.
OS Desulfococcus baarsii (Desulfovibrio baarsii).
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=887;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=DSM 2075;
RC MEDLINE=97113430; PubMed=8955290;
RX Planzolla M.J., Soubes M., Touati D.;
RA "Overproduction of rbo gene product from Desulfovibrio species
RT suppresses all deleterious effects of lack of superoxide dismutase in
RT Escherichia coli.";
RL J. Bacteriol. 178:6736-6742(1996).
DR EMBL; X99543; CAA67881.1; -.
DR HSPG; P00269; IRB9.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR004039; Rubredox.
DR Pfam; PF001052; Rubredoxin.
DR Pfam; PF00301; rubredoxin; 1.
DR PRINTS; PR00163; RUBREDOXIN.
DR ProDom; PD001610; Rubredoxin; 1.
DR PROSITE; PS00202; RUBREDOXIN; 1.
DR PROSITE; PS00903; RUBREDOXIN LIKE; 1.
SQ SEQUENCE 53 AA; 5645 MW; 3EA3C9D055F84CB0 CRC64;

Query Match 66.7%; Score 4; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
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|
DB 35 ADWS 38

RESULT 26
Q9XPF8 PRELIMINARY; PRT; 54 AA.

ID Q9XPF8 AC Q9XPF8; (T-EMBLrel. 12, Created)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Adenosine triphosphatase subunit 8.
GN ATPAS8.
GN Gonostoma gracile (Slender fangjaw).
OS Mitochondrion.
OG Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Stomiformes; Gonostomatidae; Gonostoma.
OX NCBI_TaxID=48457;

[1]
RN SEQUENCE FROM N.A.
RP PubMed=10525676;
RA Miya M., Nishida M.;
RT "Organization of the mitochondrial genome of a deep-sea fish,
RT Gonostoma gracile (Teleostei: Stomiformes): First example of transfer
RL RNA gene rearrangements in bony fishes.";
Mar. Biotechnol. 1:416-426(1999).
DR EMBL; AB016274; BAA82489.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR001421; ATPase8 mit.
DR Pfam; PF00895; ATP-synt_8; 1.
KW Mitochondrion.
SQ SEQUENCE 54 AA; 6308 MW; 66E15951E26295FE CRC64;

Query Match 66.7%; Score 4; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSW 5
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DB 50 DMSW 53

RESULT 27
R84RU5 PRELIMINARY; PRT; 57 AA.

ID R84RU5 AC R84RU5; (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE P0571D04.19 protein.
GN P0571D04.19.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Nipponbare;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GR3) genomic DNA, chromosome 7, PAC
RT clone:P0571D04.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AP004315; BAC65933.1; -.
SQ SEQUENCE 57 AA; 6370 MW; E09B7BA2BD419F0D CRC64;

Query Match 66.7%; Score 4; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSW 5
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DB 14 DMSW 17

RESULT 28
R8YQ61 PRELIMINARY; PRT; 57 AA.

ID R8YQ61 AC R8YQ61; (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein AS13974.
GN AS13974.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
[1]
RN SEQUENCE FROM N.A.
RP

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RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain FCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003594; BAB75673.1; -.
DR PIR; AG2302; AG2302.
DR InterPro; IPR003756; DUF172.
DR InterPro; IPR006442; Phd_fam.
DR Pfam; PF02604; DUF172; 1.
DR TRNFRFAM; TIGR01552; phd_fam; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 57 AA; 6335 MW; CBC5DEC16952550F CRC64;

Query Match 66.7%; Score 4; DB 16; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 41 ADWS 44

RESULT 29
Q7UG12 Q7UG12 PRELIMINARY; PRT; 65 AA.
AC Q7UG12;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN R55207.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schleiner H., Anann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294141; CAD78347.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 65 AA; 7409 MW; 34A78BF2B514A7FE CRC64;

Query Match 66.7%; Score 4; DB 16; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 28 ADWS 31

RESULT 30
Q99QG6 Q99QG6 PRELIMINARY; PRT; 74 AA.
AC Q99QG6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCF1.348.
GN SCF1.348 AND SCF1.06C.
OS Streptomyces coelicolor.

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OG Plasmid SCP1.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rebbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)."
RL Nature 417:141-147(2002).
DR EMBL; AL590464; CAC36873.1; -.
DR EMBL; AL590463; CAC36528.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 74 AA; 7940 MW; 48C43E8075052C08 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 74;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 32 WSWA 35

RESULT 31
Q862X5 Q862X5 PRELIMINARY; PRT; 76 AA.
AC Q862X5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Similar to C10 protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22544902; PubMed=12658628;
RA Ishiwata H., Katsuma S., Kizaki K., Patel O.V., Nakano H.,
RA Takahashi T., Imai K., Hirasawa A., Shiojima S., Ikawa H., Suzuki Y.,
RA Tsujimoto G., Izaike Y., Todoroki J., Haeizume K.;
RT "Characterization of gene expression profiles in early bovine
RT pregnancy using a custom cDNA microarray."
RL Mol. Reprod. Dev. 65:9-18(2003).
DR EMBL; AB098775; BAC56311.1; -.
FT NON_TER 1
FT NON_TER 76
SQ SEQUENCE 76 AA; 8339 MW; 261DDF331051EAD4 CRC64;

Query Match 66.7%; Score 4; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 27 ADWS 30

RESULT 32
Q7UUN4

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ID Q7UUN4 PRELIMINARY; PRT; 77 AA.
AC Q7UUN4;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB3190.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294138; CAD73045.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 77 AA; 9150 MW; FAB9BA1713CD432 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 68 ADWS 71

RESULT 33
Q7UGR5 PRELIMINARY; PRT; 77 AA.
AC Q7UGR5;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB5062.
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294141; CAD78264.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 77 AA; 8603 MW; 1463926B0338815C CRC64;

Query Match 66.7%; Score 4; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 14 ADWS 17

RESULT 34
Q7V158 PRELIMINARY; PRT; 82 AA.
ID Q7V158

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AC Q7V158;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Conserved hypothetical.
GN PMM1028.
OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642;
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.B., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19487.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 82 AA; 9368 MW; D5EC78F79859EDA3 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 82;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 22 ADWS 25

RESULT 35
Q8FBL8 PRELIMINARY; PRT; 85 AA.
ID Q8FBL8
AC Q8FBL8;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN C4754.
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR EMBL; AE016769; AAN83187.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 85 AA; 9675 MW; 47DADB502F570A8B CRC64;

Query Match 66.7%; Score 4; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSW 5
DB 20 DWSW 23

RESULT 36
Q8HA12

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ID Q8HA12 PRELIMINARY; PRT; 87 AA.
AC Q8HA12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OF-87.
GN OF-87.
OS Salmonella typhimurium bacteriophage Sf64T.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OC NCBI_TaxID=173443;
RN [1]
RP SEQUENCE FROM N.A.
RA Mmolawa P.T., Thomas C.J., Heuzenroeder M.W.;
RT "Sequence of the genome of Salmonella enterica serovar Typhimurium
bacteriophage Sf64T."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052766; AA115484.1; -.
SQ SEQUENCE 87 AA; 9477 MW; C0284919FB92ADC2 CRC64;

Query Match 66.7%; Score 4; DB 9; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 59 ADWS 62

RESULT 37
Q97SD6 PRELIMINARY; PRT; 88 AA.
ID Q97SD6;
AC Q97SD6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SP0448.
GN SP0448.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetelin H., Nelson K.B., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapflee E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang P., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AE007356; AAK74609.1; -.
DR PIR; H95051; H95051.
DR TIGR; SP0448; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 10274 MW; 0E3E79C00C7DD2F2 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 18 ADWS 21

RESULT 38
Q8C262 PRELIMINARY; PRT; 88 AA.
ID Q8C262;
AC Q8C262;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN SP0404.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21429245; PubMed=11544234;
RX Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Batrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6."
RL J. Bacteriol. 183:5709-5717(2001).
DR EMBL; AE008420; AAK99208.1; -.
DR PIR; D97922; D97922.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 88 AA; 10292 MW; 0E2215B011413435 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 18 ADWS 21

RESULT 39
Q9F925 PRELIMINARY; PRT; 90 AA.
ID Q9F925;
AC Q9F925;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Serratia entomophila.
GN Plasmid PADAP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OC NCBI_TaxID=42906;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ALMO2;
RX MEDLINE=20416224; PubMed=10960097;
RA Hurst M.R., Glare T.R., Jackson T.A., Ronson C.W.;
RT "Plasmid-located pathogenicity determinants of Serratia entomophila,
the causal agent of amber disease of grass grub, show similarity to
the insecticidal toxins of Photobacterium luminescens."
RL J. Bacteriol. 182:5127-5138(2000).
DR EMBL; AF135182; AAC09646.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR008473; DUF754.
DR PIR; P05449; DUF754; 1.
DR PIR; P05449; DUF754; 1.
KW Hypothetical protein; plasmid.
SQ SEQUENCE 90 AA; 10415 MW; CC3B9A4266B9EAA1 CRC64;

Query Match 66.7%; Score 4; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

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Db          61 ADWS 64
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PRELIMINARY;      PRT;      92 AA.
Q8H6W2:
AC Q8H6W2: 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gag-protease polypeptide-like protein (Fragment).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. ICC4958;
RA Benko-Iseppon A.N., Winter P., Huettel B., Kahl G., Stagginus C.,
RA Muehlbauer F.;
RT "Fine Mapping of Fusarium Resistance in Chickpea (Cicer arietinum L.)
RT using DAF (DNA Amplification Fingerpringing).";
RL Theor. Appl. Genet. 0:0-0(2003).
DR EMBL; AF457593; AAN06609.1; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
KW Polyprotein; Protease.
FT NON_TER 1
FT NON_TER 92
SQ SEQUENCE 92 AA; 10030 MW; 98AC81FAF2A958D5 CRC64;

Query Match      66.7%; Score 4; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||||
DB 68 ADWS 71

PRELIMINARY;      PRT;      93 AA.
Q939G8:
AC Q939G8: 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ypa4.
OS Pseudomonas alcaligenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=43263;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 55044;
RA Vaisvilla R., Morgan R.D., Posfai J., Raleigh E.A.;
RT "Discovery and Distribution of Super-Integrans among Pseudomonads.";
RL Mol. Microbiol. 0:0-0(2001).
DR EMBL; AY038186; AAK73290.1; -.
SQ SEQUENCE 93 AA; 10221 MW; 510C511AB8065D5D CRC64;

Query Match      66.7%; Score 4; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
|||||
DB 64 ADWS 67

PRELIMINARY;      PRT;      94 AA.
Q39643:
AC Q39643: 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lectin (Fragment).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=96104306; PubMed=8564304;
RA Toyama T., Takekoshi H., Takeba G., Tsuji H.;
RT "Cytokinin induces a rapid decrease in the levels of mRNAs for
RT catalase, 3-hydroxy-3-methylglutaryl CoA reductase, lectin and other
RT unidentified proteins in etiolated cotyledons of cucumber.";
RL Plant Cell Physiol. 36:1349-1359(1995).
DR EMBL; D63388; BAA09704.1; -.
DR PIR; T10250; T10250.
FT NON_TER 1
FT NON_TER 94
SQ SEQUENCE 94 AA; 10947 MW; 50D6958B40E35C4D CRC64;

Query Match      66.7%; Score 4; DB 10; Length 94;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
|||||
DB 35 WSWA 38

PRELIMINARY;      PRT;      95 AA.
Q9YT75:
AC Q9YT75: 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S3V3-6;
RX MEDLINE=98445411; PubMed=9770526;
RA Markham R.B., Wang W.C., Weisstein A.E., Wang Z., Munoz A.,
RA Templeton A., Margolick J., Vlahov D., Quinn T., Farzadegan H.,
RA Yu X.F.;
RT "Patterns of HIV-1 evolution in individuals with differing rates of
RT CD4 T cell decline.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:12568-12573(1998).
DR EMBL; AF089118; AAC79058.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIMS; Coat protein; Glycoprotein.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10821 MW; 5AED906D634FFE82 CRC64;

Query Match      66.7%; Score 4; DB 15; Length 95;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
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Db          67 ADWS 70

RESULT 44
Q7U4Q9
ID Q7U4Q9 PRELIMINARY; PRT; 96 AA.
AC Q7U4Q9
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical
GN SYN2005
OS Synecococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641;
RA Palenik B., Brahamsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerine J., Regala W., Allen E.E., McCarron J., Paulsen I.,
RA Dufrene A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569694; CA808520.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA; 10936 MW; 1C752C8175DFEC45 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 96;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 WSWA 6
Db          78 WSWA 81

RESULT 45
Q8AA86
ID Q8AA86 PRELIMINARY; PRT; 98 AA.
AC Q8AA86
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative thioredoxin.
GN BT0549.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=8118;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016928; AA075656.1; -
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006663; Thioredox_dom2.
KW Complete proteome.
SQ SEQUENCE 98 AA; 11466 MW; 133C672116BB881C CRC64;

Query Match 66.7%; Score 4; DB 16; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 ADWS 4
Db          23 ADWS 26

RESULT 46
Q9JRI6
ID Q9JRI6 PRELIMINARY; PRT; 100 AA.
AC Q9JRI6
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA0684.
GN NMA0684 OR NMB1782.
OS Neisseria meningitidis (serogroup A), and
OS Neisseria meningitidis (serogroup B), and
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699, 491, 487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=22491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.";
RL Nature 404:502-506(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gunn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Citton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=22491 / Serogroup A / Serotype 4A, AND FAM18;
RX MEDLINE=20187481; PubMed=10722605;
RA Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
RA Tinsley C.R.;
RT "Molecular and biological analysis of eight genetic islands that distinguish neisseria meningitidis from the closely related pathogen Neisseria gonorrhoeae.";
RL Infect. Immun. 68:2082-2095(2000).
DR EMBL; AL162753; CAB83970.1; -
DR EMBL; AB002528; AAF42122.1; -
DR EMBL; AJ391255; CAB71942.1; -
DR EMBL; AJ391284; CAB72071.1; -
DR PIR; H81042; H81042.
DR TIGR; NMB1782; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 100 AA; 10887 MW; 7D87B18A310B89C3 CRC64;

Query Match 66.7%; Score 4; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 DWSW 5
Db          77 DWSW 80

RESULT 47

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Q82UA8	PRELIMINARY;	PRT;	100 AA.
ID	Q82UA8		
AC	Q82UA8;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Hypothetical protein.		
GN	NEI598		
OS	Nitrosomonas europaea.		
OC	Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;		
OC	Nitrosomonadaceae; Nitrosomonas.		
OX	NCBI_TaxID=915;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 19718 / IF0 14298;		
RX	MEDLINE=22586410; PubMed=12700255;		
RA	Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.,		
RA	Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,		
RA	Arriero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;		
RA	"Complete genome sequence of the ammonia-oxidizing bacterium and		
RT	obligate chemolithoautotroph Nitrosomonas europaea.";		
RL	J. Bacteriol. 185:2759-2773(2003).		
DR	EMBL; BX321861; CAD85499.1; -.		
DR	Hypothetical protein; Complete proteome.		
SK	SEQUENCE 100 AA; 11563 MW; A067551AA5350CD0 CRC64;		
QW			
Query Match	66.7%; Score 4; DB 16; Length 100;		
Best Local Similarity	100.0%; Pred. No. 4.2e+02;		
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ADWS 4		
DB	36 ADWS 39		
RESULT 48			
Q8GSE6	PRELIMINARY;	PRT;	101 AA.
ID	Q8GSE6		
AC	Q8GSE6;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)		
DE	P0438G07.16 protein (B1126F07.16 protein).		
GN	P0438G07.16 OR B1126F07.16.		
OS	Oryza sativa (japonica cultivar-group).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
OC	Ehrhartoideae; Magnoliaceae; Oryzoideae; Oryza.		
OX	NCBI_TaxID=39947;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Yamamoto K.;		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, PAC		
RT	clone:P0438G07.";		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=cv. Nipponbare;		
RA	Sasaki T., Matsumoto T., Katayose Y.;		
RT	"Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC		
RT	clone:B1126F07.";		
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF004398; BAC22373.1; -.		
DR	EMBL; AF005674; BAC22484.1; -.		
SQ	SEQUENCE 101 AA; 10894 MW; 2C12C798D110A081 CRC64;		
Query Match	66.7%; Score 4; DB 10; Length 101;		
Best Local Similarity	100.0%; Pred. No. 4.2e+02;		
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 ADWS 4		

FT NON TER 103 103
SQ SEQUENCE 103 AA; 11690 MW; 0534281AAAC29CA4 CRC64;
Query Match 66.7%; Score 4; DB 12; Length 103;
Best Local Similarity 100.0%; Pred.No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 WSWA 6
Db 65 WSWA 68

Search completed: July 23, 2004, 13:26:12
Job time : 64 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:21:20 ; Search time 14 Seconds
(without alignments)
22.316 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADMSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	470	1	NRAM_IADBU Q07570 influenza a
2	5	83.3	470	1	NRAM_IADCH Q07571 influenza a
3	5	83.3	470	1	NRAM_IADH2 Q07572 influenza a
4	5	83.3	470	1	NRAM_IADM2 Q07573 influenza a
5	5	83.3	470	1	NRAM_IADFN Q07574 influenza a
6	5	83.3	470	1	NRAM_IADGD Q07577 influenza a
7	5	83.3	470	1	NRAM_IADHI Q07578 influenza a
8	5	83.3	470	1	NRAM_IADIE Q07583 influenza a
9	5	83.3	470	1	NRAM_IADKL Q07585 influenza a
10	5	83.3	470	1	MRJ5_APIME Q07432 epis mellif
11	5	83.3	598	1	LCCB_LEUME P81052 leuconostoc
12	4	66.7	31	1	TXD3_PARLU P83258 paracelote
13	4	66.7	36	1	TXD1_PARLU P83256 paracelote
14	4	66.7	37	1	TXD1_PARLU P86543 mycobacteri
15	4	66.7	93	1	ACYF_MYCTU Q8K998 buchnera ap
16	4	66.7	114	1	Y451_BUCAP Q94502 bacillus su
17	4	66.7	128	1	YRDN_BACSU O64223 mycobacteri
18	4	66.7	147	1	VG29_BPMD2 O52336 mycobacteri
19	4	66.7	147	1	YB19_PSPPK Q88nt5 pseudomonas
20	4	66.7	160	1	YB19_PSPPK Q97n33 streptococ
21	4	66.7	169	1	YB19_PSPPK Q88nt5 pseudomonas
22	4	66.7	169	1	YB19_PSPPK Q97n33 streptococ
23	4	66.7	182	1	RL18_HALN1 P10888 rattus norv
24	4	66.7	197	1	YB21_AQUAE P50562 halobacteri
25	4	66.7	200	1	HAM1_STRPN Q67415 aquifex ao
26	4	66.7	208	1	TATB_XANAC Q88nt5 pseudomonas
27	4	66.7	213	1	RECN_PAVEO Q88nt5 pseudomonas
28	4	66.7	227	1	RECO_PSEAE Q88nt5 pseudomonas
29	4	66.7	233	1	UBIE_LISWO Q92a77 listeria mo
30	4	66.7	237	1	UBIE_LISWO Q92a77 listeria mo
31	4	66.7	256	1	TAM_RHILO Q98k73 rhizobium l
32	4	66.7	257	1	YK09_RALSO Q88xv4 ralsconia s
33	4	66.7	262	1	DET2_ARATH Q88944 arabidopsis

34	4	66.7	272	1	CY1_RHORU	P23135 rhodospiril
35	4	66.7	279	1	HRP5_HUMAN	Q96ku8 homo sapien
36	4	66.7	280	1	CHR2_PSEAE	Q916v7 pseudomonas
37	4	66.7	282	1	3MG2_ECOLI	P40395 escherichia
38	4	66.7	284	1	RP32_PSEAE	P42378 pseudomonas
39	4	66.7	289	1	POR1_RHOBL	P39767 rhodopseudo
40	4	66.7	291	1	C552_PSEST	P24037 pseudomonas
41	4	66.7	295	1	RSP4_BOVIN	P26452 bos taurus
42	4	66.7	295	1	RSP4_CRIGR	P38982 cricetus
43	4	66.7	295	1	RSP4_HUMAN	P08865 homo sapien
44	4	66.7	295	1	RSP4_MOUSE	P14206 mus musculu
45	4	66.7	295	1	RSP4_RAT	P38983 rattus norv
46	4	66.7	296	1	RSP4_CHICK	P50890 gallus gall
47	4	66.7	302	1	DHMA_CAUCR	Q9a919 caulobacter
48	4	66.7	304	1	NXP4_RAT	Q92214 rattus norv
49	4	66.7	307	1	CRTE_ERWHE	P22873 erwinia her
50	4	66.7	308	1	NXP4_HUMAN	Q95158 homo sapien
51	4	66.7	319	1	FMT_TREPA	O83737 treponema p
52	4	66.7	319	1	DUS_AZOB	P45672 azospirillu
53	4	66.7	321	1	LAD2_ENTFA	Q833w8 enterococcu
54	4	66.7	322	1	DUSA_XYLFT	Q87ay2 xylella fas
55	4	66.7	340	1	DUSA_XYLFT	Q9p9b5 xylella fas
56	4	66.7	346	1	PSTS_ECOLI	P06128 escherichia
57	4	66.7	347	1	HEM2_CAUCR	P57777 caulobacter
58	4	66.7	347	1	OXDA_HUMAN	P14920 homo sapien
59	4	66.7	347	1	OXDA_RABIT	P22942 oryctolagus
60	4	66.7	348	1	GTOM_ARATH	Q9zsk1 arabidopsis
61	4	66.7	351	1	DESA_SYNY3	P20388 synecocyst
62	4	66.7	354	1	ALKB_ARATH	Q9sa98 arabidopsis
63	4	66.7	360	1	WNT2_CABEL	P34899 caenorhabdi
64	4	66.7	361	1	YB19_SYNY3	P73341 synecocyst
65	4	66.7	362	1	DCUP_YEAST	P23347 saccharomyc
66	4	66.7	363	1	PSPB_CANFA	P17129 canis fami
67	4	66.7	364	1	PSTS_XYLFA	Q9pbk3 xylella fas
68	4	66.7	364	1	PSTS_XYLFT	Q87c91 xylella fas
69	4	66.7	375	1	PEX7_YEAST	P39108 saccharomyc
70	4	66.7	376	1	PGLR_PENGR	O3883 penicillium
71	4	66.7	380	1	Y378_HALN1	Q9hs70 halobacteri
72	4	66.7	394	1	PKR_BACST	P18912 bacillus st
73	4	66.7	394	1	TGT_DEIRA	Q9rb5 deinococcus
74	4	66.7	399	1	PKD_ASCSU	O02623 ascaris suu
75	4	66.7	401	1	BMP4_XENLA	P30895 xenopus lae
76	4	66.7	401	1	PKD_CABEL	Q02332 caenorhabdi
77	4	66.7	409	1	AXIA_BRARE	Q07342 brachydanio
78	4	66.7	411	1	FOLC_BUCAI	P57265 buchnera ap
79	4	66.7	413	1	YTH1_PANTH	P46351 paenibacill
80	4	66.7	416	1	TRH3_CHICK	P18519 gallus gall
81	4	66.7	437	1	YTH3_RHOER	P46372 rhodococcu
82	4	66.7	439	1	TSAT_TAXCH	Q8896 taxus chine
83	4	66.7	439	1	TSAT_TAXCU	Q9m6f0 taxus cuspi
84	4	66.7	445	1	YKAB_BACPF	P30268 bacillus ps
85	4	66.7	452	1	CBL1_ARATH	Q9sr7 arabidopsis
86	4	66.7	453	1	NRAM_IAWIL	P03470 influenza a
87	4	66.7	454	1	NRAM_IAPUE	P03468 influenza a
88	4	66.7	460	1	HEMN_PSEAE	P77915 pseudomonas
89	4	66.7	467	1	MURD_BRUME	Q9y168 brucella me
90	4	66.7	467	1	MURD_BRUSU	Q8fz22 brucella su
91	4	66.7	471	1	MANC_KLEPN	Q48462 klebsiella
92	4	66.7	471	1	MURD_CAUCR	O9a597 caulobacter
93	4	66.7	471	1	RFM9_ECOLI	P37753 escherichia
94	4	66.7	474	1	CBF5_SCHPO	O14007 schizosacch
95	4	66.7	477	1	Y264_SYNY3	P73436 synecocyst
96	4	66.7	483	1	LIA2_HUMAN	Q8n149 homo sapien
97	4	66.7	484	1	SGAT_ECOLI	P39301 escherichia
98	4	66.7	487	1	YK75_MYCTU	O10683 mycobacteri
99	4	66.7	488	1	PAC2_RAT	Q9qv17 rattus norv
100	4	66.7	491	1	G6PD_BUCAI	P57405 buchnera ap
101	4	66.7	501	1	GUAA_THEME	Q9x280 thermotoga
102	4	66.7	501	1	PLI3_ARATH	Q93204 arabidopsis
103	4	66.7	505	1	GUAA_PYRAE	Q8t592 pyrobaculum
104	4	66.7	526	1	GUAA_STRCO	Q910h2 streptomyce
105	4	66.7	547	1	OM6C_CHLTR	P26758 chlamydia t
106	4	66.7	547	1	OM6D_CHLTR	P18151 chlamydia t

107	4	66.7	547	1	OM6E_CHLTR	P23603	chlamydia t	180	4	66.7	1107	1	POL2_RRVS	P36324	raspberry r
108	4	66.7	547	1	OM6L_CHLTR	P21354	chlamydia t	181	4	66.7	1125	1	YB62_SCHPO	O14248	schizosacch
109	4	66.7	550	1	VGLE_HSV1	P04488	herpes simp	182	4	66.7	1230	1	UGS4_SOLTU	O43846	schizosacch
110	4	66.7	552	1	GPM1_LEPIN	P59173	leptospiro	183	4	66.7	1259	1	YTFN_ECOLI	P39321	escherichia
111	4	66.7	556	1	OM6_CHLPS	P23700	chlamydia p	184	4	66.7	1331	1	MANE_CALSA	P22533	caldocellum
112	4	66.7	557	1	OM6_CHLPS	P23701	chlamydia p	185	4	66.7	1423	1	FRUN_STRMU	O03174	streptococc
113	4	66.7	567	1	IP37_SCHPO	O94236	schizosacch	186	4	66.7	1573	1	ARO1_SCHPO	O90710	s pentafunc
114	4	66.7	570	1	IPFAS_ANASP	O820C1	anabaena sp	187	4	66.7	1616	1	RRPO_TWOB	P90211	tobamovirus
115	4	66.7	578	1	HASI1_HUMAN	O82839	homo sapien	188	4	66.7	1742	1	GUHA_CALSA	P22534	caldocellum
116	4	66.7	579	1	YC12_KLEPN	O48458	klebsiella	189	4	66.7	1742	1	MYHB_CHICK	P10587	gallus gall
117	4	66.7	583	1	HASI1_MOUSE	Q81647	mus musculus	190	4	66.7	3175	1	RPOA_EAV	P19811	equine arte
118	4	66.7	597	1	PEPX_BACAA	Q81647	mus musculus	191	4	66.7	3421	1	TEGU_HSVB	P28955	equine herp
119	4	66.7	601	1	DNJM_MYCGE	Q81647	mus musculus	192	4	66.7	6884	1	RIAB_CVPPU	Q91W06	p replicase
120	4	66.7	608	1	PHAC_METEX	P52070	methylobact	193	3	50.0	10	1	AKHX_LOEMI	F81626	locusta mig
121	4	66.7	608	1	UL27_HCMVA	P16763	human cytom	194	3	50.0	14	1	MAST_VESBA	P21654	vespa basal
122	4	66.7	626	1	SAD1_HUMAN	Q9Y323	homo sapien	195	3	50.0	27	1	PSBY_FUCVE	Q9BAC7	fucus vesic
123	4	66.7	630	1	Y242_MYCGE	Q9Y323	homo sapien	196	3	50.0	32	1	PSB2_EUGVI	O8E187	euglena vir
124	4	66.7	648	1	AMOI_ARTS1	P47484	mycoplasma	197	3	50.0	35	1	PSBY_CYAME	O85961	cyanidiosch
125	4	66.7	648	1	AMOI_ARTS1	Q07121	arthrobacte	198	3	50.0	36	1	PSBY_OOSI	P49543	odontella s
126	4	66.7	671	1	AMOI_ARTS1	Q07123	arthrobacte	199	3	50.0	36	1	PSBY_PORPU	F51206	porphyra pu
127	4	66.7	675	1	AMOI_ARTS1	Q9UDV7	homo sapien	200	3	50.0	37	1	PSBY_GYATH	O19893	cyamidium c
128	4	66.7	689	1	MEA_ARATH	P33215	mus musculus	201	3	50.0	37	1	PSBY_GYATH	O78433	guillardia
129	4	66.7	692	1	YKOE_YEAST	O65312	arabidopsis	202	3	50.0	37	1	TXD4_PARLU	P83259	paracoele
130	4	66.7	698	1	TR85_YEAST	P36062	saccharomyc	203	3	50.0	37	1	TXM2_AGEAP	P11058	agelenopsis
131	4	66.7	700	1	TR85_YEAST	P46944	saccharomyc	204	3	50.0	37	1	TXM4_AGEAP	P11058	agelenopsis
132	4	66.7	702	1	YKOE_YEAST	P29719	paenibacill	205	3	50.0	37	1	TXM5_AGEAP	P11061	agelenopsis
133	4	66.7	705	1	YKOE_YEAST	Q16959	anthocidari	206	3	50.0	37	1	TXM6_AGEAP	P11062	agelenopsis
134	4	66.7	715	1	YKOE_YEAST	P22699	dictyosteli	207	3	50.0	38	1	TXC2_HOLCU	P60177	hololena cu
135	4	66.7	716	1	YKOE_YEAST	P47983	canis fami	208	3	50.0	38	1	TXC3_HOLCU	P15968	hololena cu
136	4	66.7	720	1	YKOE_YEAST	P47984	felis silve	209	3	50.0	38	1	TXM3_AGEAP	P60178	agelenopsis
137	4	66.7	730	1	YKOE_YEAST	P42512	pseudomonas	210	3	50.0	40	1	ALF_CANAL	O9URB4	candida alb
138	4	66.7	730	1	YKOE_YEAST	P55303	aspergillus	211	3	50.0	40	1	YC04_ARCFU	O29084	archaeoglob
139	4	66.7	739	1	YKOE_YEAST	P26224	clostridium	212	3	50.0	43	1	PSBY_SYNXP	P59908	synechococc
140	4	66.7	743	1	YKOE_YEAST	Q98NN7	rhizobium l	213	3	50.0	44	1	PIS1_CARPI	P80569	carnobacter
141	4	66.7	745	1	YKOE_YEAST	O15111	h inhibitor	214	3	50.0	45	1	AT12_HSV2	Q00041	equine herp
142	4	66.7	745	1	YKOE_YEAST	O60680	m inhibitor	215	3	50.0	49	1	LYC_HSV2	P21776	pseudocoeir
143	4	66.7	757	1	YKOE_YEAST	O4920	homo sapien	216	3	50.0	52	1	RUBR_DSVM	P00269	desulfovibr
144	4	66.7	757	1	YKOE_YEAST	Q88351	mus musculus	217	3	50.0	52	1	RUBR_DSVM	P15412	desulfovibr
145	4	66.7	757	1	YKOE_YEAST	Q9GY78	rattus norv	218	3	50.0	52	1	RUBR_HELMO	P56283	heliobacill
146	4	66.7	757	1	YKOE_YEAST	Q9GY78	rattus norv	219	3	50.0	52	1	RUBR_MEGL	P00271	megaspheara
147	4	66.7	761	1	YKOE_YEAST	Q8Q3H8	streptococc	220	3	50.0	53	1	VG87_BPM15	Q05304	mycobacteri
148	4	66.7	773	1	YKOE_YEAST	Q8Q3H8	streptococc	221	3	50.0	54	1	CH03_CHICK	P30442	mesocricetu
149	4	66.7	783	1	YKOE_YEAST	P17201	acetobacter	222	3	50.0	54	1	B2MG_MSAU	P40667	gallus gall
150	4	66.7	810	1	YKOE_YEAST	Q82849	rattus norv	223	3	50.0	54	1	VG87_BPM2	O64268	mycobacteri
151	4	66.7	813	1	YKOE_YEAST	P34418	caenorhabdi	224	3	50.0	55	1	ATP8_RHEAM	P79396	rhea ameri
152	4	66.7	835	1	YKOE_YEAST	Q9C0E0	arabidopsis	225	3	50.0	56	1	SOX1_PLEWA	O37839	pleurodeles
153	4	66.7	836	1	YKOE_YEAST	Q9C0E0	arabidopsis	226	3	50.0	58	1	IE12_HSV2	P14345	herpes simp
154	4	66.7	862	1	YKOE_YEAST	Q13724	homo sapien	227	3	50.0	59	1	IVBI_DENAN	P00980	dendroaspis
155	4	66.7	891	1	YKOE_YEAST	P96142	thermus the	228	3	50.0	59	1	SCKD_LEIOH	P45628	leirus qui
156	4	66.7	895	1	YKOE_YEAST	P27968	hordeum vul	229	3	50.0	60	1	RUBA_RHOER	O9AE66	rhodococcus
157	4	66.7	910	1	YKOE_YEAST	Q59097	alcaligenes	230	3	50.0	62	1	YMF8_ECOLI	P75979	escharichia
158	4	66.7	911	1	YKOE_YEAST	Q8K9Y2	buchnera ap	231	3	50.0	63	1	SIX4_BUTSI	P82814	buthus sind
159	4	66.7	911	1	YKOE_YEAST	P39868	brassica na	232	3	50.0	63	1	RUB2_RHOER	Q9AE63	rhodococcus
160	4	66.7	917	1	YKOE_YEAST	P41257	campylobact	233	3	50.0	64	1	YACG_SALTY	P8AE63	rhodococcus
161	4	66.7	929	1	YKOE_YEAST	Q87137	schizosacch	234	3	50.0	64	1	ENPP_BPPA2	Q8xfv1	salmonella
162	4	66.7	944	1	YKOE_YEAST	Q97142	rhizobium l	235	3	50.0	65	1	YK20_GUITH	P10438	bacterioph
163	4	66.7	948	1	YKOE_YEAST	Q53245	rhizobium t	236	3	50.0	65	1	YK20_GUITH	O78445	guillardia
164	4	66.7	977	1	YKOE_YEAST	Q9UPU5	homo sapien	237	3	50.0	65	1	YACG_ECOLI	P05998	bacterioph
165	4	66.7	983	1	YKOE_YEAST	P29318	gallus gall	238	3	50.0	65	1	UL90_HCMVA	Q8f157	escharichia
166	4	66.7	983	1	YKOE_YEAST	P29320	homo sapien	239	3	50.0	66	1	PSBH_ODOSI	P16796	human cytom
167	4	66.7	983	1	YKOE_YEAST	P29319	mus musculus	240	3	50.0	67	1	PSBH_ODOSI	P49475	odontella s
168	4	66.7	994	1	YKOE_YEAST	O8680	rattus norv	241	3	50.0	69	1	RUB1_CHLTE	P58992	chlorobium
169	4	66.7	994	1	YKOE_YEAST	Q9PH12	xyella fas	242	3	50.0	71	1	NKLL_NAME	P01383	naja melano
170	4	66.7	1036	1	YKOE_YEAST	Q87f36	xyella fas	243	3	50.0	71	1	YE90_HASIN	P44246	haemophilus
171	4	66.7	1039	1	YKOE_YEAST	O8684	cricetulus	244	3	50.0	72	1	ATP8_METSE	O47923	metridium s
172	4	66.7	1039	1	YKOE_YEAST	P10474	c endogluca	245	3	50.0	73	1	YVAI_VACCC	P20518	vaccinia vi
173	4	66.7	1057	1	YKOE_YEAST	P55517	rhizobium s	246	3	50.0	74	1	SMS2_MYOSC	P09876	myoxocephal
174	4	66.7	1057	1	YKOE_YEAST	P18293	mus musculus	247	3	50.0	75	1	REGB_PSEAE	Q01381	pseudomonas
175	4	66.7	1061	1	YKOE_YEAST	P18910	rattus norv	248	3	50.0	78	1	IAAL_STRGS	Q01093	streptomyc
176	4	66.7	1074	1	YKOE_YEAST	P16066	homo sapien	249	3	50.0	79	1	NU5M_MACFA	P50665	macaca fasc
177	4	66.7	1074	1	YKOE_YEAST	Q13393	homo sapien	250	3	50.0	80	1	Y14C_BPT4	P39066	bacterioph
178	4	66.7	1074	1	YKOE_YEAST	P70496	rattus norv	251	3	50.0	81	1	HPIS_TH1PF	P00263	thiocapsa p
179	4	66.7	1097	1	YKOE_YEAST	P42702	homo sapien	252	3	50.0	82	1	HPIS_MARPU	P59860	marichromat

253	3	50.0	84	1	YC20_GALSU	P48409	galdieria s	326	3	50.0	108	1	Y095_ARCFU	O30141	archaeoglob
254	3	50.0	84	1	D119_HUMAN	Qn690	homo sapien	327	3	50.0	108	1	YML2_THIPE	P20088	thiobacillu
255	3	50.0	85	1	YHDT_HAEIN	P46455	haemophilus	328	3	50.0	108	1	YNFA_SALTI	Q82622	salmonella
256	3	50.0	86	1	TRBE_ECOLI	Q05807	escherichia	329	3	50.0	109	1	BPBF_BURCE	P73332	burkholderi
257	3	50.0	88	1	IE12_HSV11	P03170	herpes simp	330	3	50.0	109	1	CYPC_STRHA	Q05368	streptomyce
258	3	50.0	88	1	YQ38_BACHD	Q9K9K7	bacillus ha	331	3	50.0	109	1	KV4D_HUMAN	P83593	homo sapien
259	3	50.0	89	1	VAP1_RIEAN	O85172	riemarella	332	3	50.0	110	1	UVRA_PARDE	P29927	paracoccus
260	3	50.0	89	1	Y4MD_RHISN	P55563	rhizobium s	333	3	50.0	110	1	YCTI_YEAST	P37265	saccharomyc
261	3	50.0	89	1	YNAX_KLEAE	Q08600	klebsiella	334	3	50.0	111	1	CYC6_ANASP	P200596	anabaena sp
262	3	50.0	90	1	VP9_BPPH6	P07581	bacterioph	335	3	50.0	111	1	CYC_ENTIN	P00075	enteromorph
263	3	50.0	90	1	Y285_PSEPK	Q88r49	pseudomonas	336	3	50.0	111	1	VPX_HV2D2	P15836	human immun
264	3	50.0	90	1	YFIM_ECOLI	P46126	escherichia	337	3	50.0	111	1	Y161_UREPA	Q9PGV3	ureaplasma
265	3	50.0	90	1	VHE3_PSSSM	Q87u5	pseudomonas	338	3	50.0	111	1	YGN2_YEAST	P53126	saccharomyc
266	3	50.0	91	1	LCIB_LACLC	P35517	lactococcus	339	3	50.0	112	1	CFP6_MYCTU	O53211	mycobacteri
267	3	50.0	91	1	THIO_THIRO	P96132	thiocapsa r	340	3	50.0	112	1	NIFW_ENTAG	Q52071	mycobacteri
268	3	50.0	91	1	YA97_STRAM	Q99V05	staphylococ	341	3	50.0	112	1	VPX_HV2D1	P71760	human immun
269	3	50.0	91	1	YFDM_ECOLI	P76509	escherichia	342	3	50.0	113	1	MEAI_PIG	Q95313	sus scrofa
270	3	50.0	92	1	B2MG_MUSCE	P55078	mus cervico	343	3	50.0	113	1	RBX2_HUMAN	O9ubf6	homo sapien
271	3	50.0	92	1	B2MG_MUSCR	P55077	mus caroli	344	3	50.0	113	1	RBX2_MOUSE	Q9wt21	mus musculus
272	3	50.0	92	1	B2MG_MUSSP	Q04714	mus spretus	345	3	50.0	114	1	GTHI_FUNHE	P30971	fundulus he
273	3	50.0	93	1	VAPD_BACNO	Q46565	bacteroides	346	3	50.0	114	1	HV2A_RABIT	P01827	oryctolagus
274	3	50.0	93	1	YQ32_MYCTU	P71931	mycobacteri	347	3	50.0	114	1	YAQD_SCHPO	Q10112	schizosacch
275	3	50.0	94	1	E566_MYCTU	P95242	mycobacteri	348	3	50.0	114	1	YJ74_AQUAE	Q67794	aquifex ao
276	3	50.0	94	1	ESXI_MYCBO	P59802	mycobacteri	349	3	50.0	115	1	CZCI_ALCEU	O44009	alcaligenes
277	3	50.0	94	1	ESXI_MYCTU	P96364	mycobacteri	350	3	50.0	115	1	MYHA_MOUSE	Q61879	mus musculus
278	3	50.0	94	1	ESXL_MYCBO	P59804	mycobacteri	351	3	50.0	115	1	NPFF_BOVIN	Q9tux7	bos taurus
279	3	50.0	94	1	ESKL_MYCTU	O05300	mycobacteri	352	3	50.0	115	1	TKN1_RABIT	P41540	oryctolagus
280	3	50.0	94	1	ESXN_MYCTU	Q53242	mycobacteri	353	3	50.0	115	1	YAT7_RHOBL	P05450	rhodopseuo
281	3	50.0	95	1	VAPD_ACTAC	O52243	actinobacil	354	3	50.0	115	1	YEAQ_ECOLI	P76243	escherichia
282	3	50.0	96	1	NEUY_BRARE	Q8i8p3	brachydanio	355	3	50.0	116	1	HV1A_RABIT	P01836	oryctolagus
283	3	50.0	96	1	YLJ4_ARCFU	O28146	archaeoglob	356	3	50.0	116	1	MSCL_STAEP	Q8cp24	staphylococ
284	3	50.0	97	1	CUB3_HSV6U	P52460	human herpe	357	3	50.0	116	1	Y162_ARCFU	Q30075	archaeoglob
285	3	50.0	97	1	CUB3_HSV6Z	P52461	human herpe	358	3	50.0	116	1	YE94_HAEIN	O05071	haemophilus
286	3	50.0	97	1	FIXX_RHISN	Q53207	rhizobium s	359	3	50.0	117	1	ARR1_ECOLI	P15905	escherichia
287	3	50.0	97	1	Y356_METJA	Q57802	methanococ	360	3	50.0	117	1	ARR2_ECOLI	P52144	escherichia
288	3	50.0	97	1	YAN9_YEAST	P39565	saccharomyc	361	3	50.0	117	1	CHBB_CROHO	P81509	crotalus ho
289	3	50.0	98	1	B2MG_MELGA	P21612	meleagris g	362	3	50.0	117	1	HV14_MOUSE	P01758	mus musculus
290	3	50.0	98	1	PHS_RHILO	Q98e92	rhizobium l	363	3	50.0	117	1	HV62_MOUSE	P18530	mus musculus
291	3	50.0	98	1	REGN_BPPH8	P06154	bacterioph	364	3	50.0	117	1	NU3M_LUMTE	Q34950	lumbricus t
292	3	50.0	98	1	VG04_BPMD2	O64200	mycobacteri	365	3	50.0	117	1	NU3M_PROWI	P37625	prototheca
293	3	50.0	98	1	VG04_BPML5	O05251	mycobacteri	366	3	50.0	118	1	ABBB_TRIAB	P81116	trimeresuru
294	3	50.0	98	1	YD22_MYCTU	Q10635	mycobacteri	367	3	50.0	118	1	B2MG_BOVIN	P01888	bos taurus
295	3	50.0	98	1	YDAS_ECOLI	P76063	escherichia	368	3	50.0	118	1	B2MG_HORSE	P30441	equus cabal
296	3	50.0	99	1	B2MG_RABIT	P01885	oryctolagus	369	3	50.0	118	1	B2MG_PIG	Q07717	sus scrofa
297	3	50.0	99	1	GP45_BSPP1	O48399	bacterioph	370	3	50.0	118	1	HV39_MOUSE	P01809	mus musculus
298	3	50.0	99	1	NOS3_SHEEP	P79209	ovis aries	371	3	50.0	118	1	V118_ASFB7	P18556	african swi
299	3	50.0	99	1	RS6_FACPL	Q990k2	lactobacill	372	3	50.0	118	1	Y380_METJA	Q57825	methanococ
300	3	50.0	99	1	YQJK_ECOLI	Q47710	escherichia	373	3	50.0	118	1	YE16_HAEIN	P44188	haemophilus
301	3	50.0	100	1	NOS3_CAVPO	P97270	cavia porce	374	3	50.0	119	1	B2MG_ALOSE	O77523	alouatta se
302	3	50.0	101	1	THI1_CHLTE	Q8kea4	chlorobium	375	3	50.0	119	1	B2MG_AOTAZ	O77537	actus azara
303	3	50.0	101	1	Y4F3_ENTFA	Q01894	enterococcu	376	3	50.0	119	1	B2MG_AOTNA	O46570	actus nancy
304	3	50.0	102	1	GTH1_THUOB	P37205	thunnus obe	377	3	50.0	119	1	B2MG_ATEPA	O77536	ateles pani
305	3	50.0	102	1	Y06M_BPFA	P32273	bacterioph	378	3	50.0	119	1	B2MG_BRAAR	O77524	brachyteles
306	3	50.0	102	1	YBEB_HAEIN	P44471	haemophilus	379	3	50.0	119	1	B2MG_CACME	O77533	cacajao mel
307	3	50.0	102	1	YNCB_BACSU	P39600	bacillus su	380	3	50.0	119	1	B2MG_CALEM	O77529	callitrich
308	3	50.0	103	1	C552_NITEU	P95339	nitrosomona	381	3	50.0	119	1	B2MG_CALHO	O77522	callitrich
309	3	50.0	103	1	HEX9_ADECT	Q65944	canine aden	382	3	50.0	119	1	B2MG_CALJA	O77522	callitrich
310	3	50.0	103	1	HEX9_ADECT	P14268	canine aden	383	3	50.0	119	1	B2MG_CALPN	O77528	callitrich
311	3	50.0	103	1	LAC_CHICK	P20763	gallus gall	384	3	50.0	119	1	B2MG_CALPP	O77536	callitrich
312	3	50.0	103	1	MMOD_METCA	P22867	methylococ	385	3	50.0	119	1	B2MG_CALTO	O77536	callitrich
313	3	50.0	103	1	Y944_PYRHO	O58672	pyrococcus	386	3	50.0	119	1	B2MG_CEBAL	O77536	cebus albif
314	3	50.0	104	1	Y019_NPVOP	O10279	orgyia pseu	387	3	50.0	119	1	B2MG_CEBPY	O77535	cebuella py
315	3	50.0	104	1	YK12_YEAST	P36127	saccharomyc	388	3	50.0	119	1	B2MG_CHISA	O77532	chiropotes
316	3	50.0	105	1	SUGE_CITFR	O69279	citrobacter	389	3	50.0	119	1	B2MG_CRIGR	O9WV24	cricetus
317	3	50.0	105	1	THI1_CORNE	P00275	corynebacte	390	3	50.0	119	1	B2MG_HUMAN	P01884	homo sapien
318	3	50.0	105	1	YBEB_ECOLI	P05848	escherichia	391	3	50.0	119	1	B2MG_LAGLA	O77525	lagothrix l
319	3	50.0	106	1	YA43_RHIME	Q92r68	rhizobium m	392	3	50.0	119	1	B2MG_LEOCH	O8spW0	leontopithe
320	3	50.0	106	1	YDFG_BACNO	P39884	bacteroides	393	3	50.0	119	1	B2MG_MACFA	Q8spW0	macaca fasc
321	3	50.0	107	1	OACH_STASA	O87868	staphylococ	394	3	50.0	119	1	B2MG_MOUSE	P01887	mus musculus
322	3	50.0	107	1	THIO_CHRVI	P09857	chromatium	395	3	50.0	119	1	B2MG_PITIR	O77531	pithecia ir
323	3	50.0	107	1	YF95_HAEIN	P44266	haemophilus	396	3	50.0	119	1	B2MG_PONPY	P16213	pongo pygma
324	3	50.0	108	1	MIDI_MUSCR	P82456	mus caroli	397	3	50.0	119	1	B2MG_RAT	O77151	rattus norv
325	3	50.0	108	1	VNEM_LVX	P27331	lily virus	398	3	50.0	119	1	B2MG_SAGBB	O77516	saguinus bi

399	1	B2MG SAGFU	119	3	50.0	119	Q7518	saguinus fu	472	3	50.0	132	1	RS11_CHLMU	Q9pj3	chlamydia m
400	1	B2MG SAGIM	119	3	50.0	119	O77517	saguinus im	473	3	50.0	132	1	RS11_CHLTR	Q7761	chlamydia t
401	1	B2MG SAGIN	119	3	50.0	119	O77518	saguinus mi	474	3	50.0	132	1	RS11_CLOTE	Q8908	clostridium
402	1	B2MG SAGE	119	3	50.0	119	P55079	saguinus oe	475	3	50.0	132	1	YBL2_STRCI	P3654	streptomyce
403	1	B2MG SAIBB	119	3	50.0	119	O77534	saimiri bol	476	3	50.0	132	1	YF83_MYCTU	O06607	mycobacteri
404	1	RNP_IGUIG	119	3	50.0	119	P80287	iguana igua	477	3	50.0	133	1	CRCB_XYLFT	Q87d8	xylella fas
405	1	YCE2_YEAST	119	3	50.0	119	P25572	saccharomyc	478	3	50.0	133	1	PABP SCHMA	P29498	schistosoma
406	1	YGE58 METJA	119	3	50.0	119	Q59052	methanococc	479	3	50.0	133	1	KV2F HUMAN	P06310	homo sapien
407	1	IAA2_STRGS	120	3	50.0	120	P20078	streptomyce	480	3	50.0	133	1	RS11_CHLPN	Q92787	chlamydia p
408	1	NU3M_DICDI	120	3	50.0	120	Q37312	dictyosteli	481	3	50.0	133	1	RS11_RALSO	O8xv36	ralstonia s
409	1	RA14_CANAL	121	3	50.0	121	P53709	candida alb	482	3	50.0	133	1	Y54L_SYNY3	P27777	synechocyst
410	1	RX11_YEAST	121	3	50.0	121	Q08273	saccharomyc	483	3	50.0	133	1	YVAD_BACSU	O32226	bacillus su
411	1	RS11_UREPA	121	3	50.0	121	Q9pgm5	ureaplasma	484	3	50.0	134	1	RS11_COREF	P59371	corynebacte
412	1	SRV_RAT	121	3	50.0	121	P36394	rattus norv	485	3	50.0	134	1	RS11_CORGL	O8nsv5	corynebacte
413	1	Y198_VERPE	121	3	50.0	121	Q8zib7	versinia pe	486	3	50.0	134	1	RS11_STRAW	Q82dm3	streptomyce
414	1	V14K_PMV	122	3	50.0	122	P20955	papaya mosa	487	3	50.0	134	1	RS11_STRCO	P72403	streptomyce
415	1	ABAA_TRIAB	123	3	50.0	123	P20955	papaya mosa	488	3	50.0	134	1	VAL3_SLVC	P29049	squash leaf
416	1	ECHB_ECHCA	123	3	50.0	123	P81996	echis carin	489	3	50.0	135	1	MSRB_AGR75	Q8ugx7	agrobacteri
417	1	IAA2_WHEAT	123	3	50.0	123	P01083	tritium ae	490	3	50.0	135	1	RS11_SHEVI	Q96070	shewanella
418	1	MECI_STRAA	123	3	50.0	123	P26598	staphylococ	491	3	50.0	135	1	VAL2_CLVNI	P14976	cassava lat
419	1	PRO2_PHYPO	124	3	50.0	124	P18322	physarum po	492	3	50.0	135	1	VAL2_TLVCM	P14968	cassava lat
420	1	ALR_HUMAN	125	3	50.0	125	P55789	homo sapien	493	3	50.0	135	1	VAL2_TLVCM	P27263	tomato yell
421	1	BOTE_BOTJA	125	3	50.0	125	P22030	bothrops ja	494	3	50.0	135	1	VAL2_TYLCU	P38610	tomato yell
422	1	SOR_ARCFU	125	3	50.0	125	O29903	archaeoglob	495	3	50.0	136	1	PSBR_TOBAC	P27262	tomato yell
423	1	VG4_BPPH2	125	3	50.0	125	P03682	bacterioph	496	3	50.0	136	1	RS11_MYCPU	Q40519	nicotiana t
424	1	VG4_BPPZA	125	3	50.0	125	P06952	bacterioph	497	3	50.0	136	1	RS11_MYCPU	Q98q07	mycoplasma
425	1	VG61_BPMD2	125	3	50.0	125	O64253	mycobacteri	498	3	50.0	136	1	Y07C_BPT4	Q98q79	homo sapien
426	1	VG61_BPML5	125	3	50.0	125	Q05274	mycobacteri	499	3	50.0	136	1	Y07C_BPT4	P13323	bacterioph
427	1	V3C2_STRCO	125	3	50.0	125	Q53868	streptomyce	500	3	50.0	136	1	Y16K_GSMV	P18919	chloris str
428	1	YNB3_YEAST	125	3	50.0	125	P53979	saccharomyc	501	3	50.0	137	1	RPB6_CAEEL	Q17684	caenorhabdi
429	1	RS11_TREPA	126	3	50.0	126	Q83241	treponema p	502	3	50.0	137	1	RR11_SPIOL	P06506	spiniacia ol
430	1	YTFH_ECOLI	126	3	50.0	126	P39316	escherichia	503	3	50.0	137	1	YMAF_BACSU	Q81794	bacillus su
431	1	THIO_NEUCR	127	3	50.0	127	P42115	neurospora	504	3	50.0	138	1	CH16_DROME	P27977	drosofila
432	1	TRG3_HUMAN	127	3	50.0	127	Q9y5p2	homo sapien	505	3	50.0	138	1	CSGF_ECOLI	P52104	escherichia
433	1	YCT3_YEAST	127	3	50.0	127	P25361	saccharomyc	506	3	50.0	138	1	R14A_YEAST	P36105	saccharomyc
434	1	YMG0_YEAST	128	3	50.0	128	Q4501	saccharomyc	507	3	50.0	138	1	R14B_YEAST	P38754	saccharomyc
435	1	IH08_HCMVA	129	3	50.0	129	P16806	human cytom	508	3	50.0	138	1	RR9_ODOSI	P49497	odontella s
436	1	NUSB_STABP	129	3	50.0	129	O8cp37	staphylococ	509	3	50.0	138	1	VGAM_LAMBD	P03702	bacterioph
437	1	RS11_BACHD	129	3	50.0	129	O50633	bacillus ha	510	3	50.0	138	1	CH16_DROVI	Q24511	drosofila
438	1	RS11_NITEU	129	3	50.0	129	Q82x71	nitrosomona	511	3	50.0	139	1	RBS_PLECA	Q08052	pleurochrys
439	1	RS11_PSEAE	129	3	50.0	129	Q9hwf8	pseudomonas	512	3	50.0	139	1	Y9E5_MYCTU	P21545	mycobacteri
440	1	RS11_PSEPK	129	3	50.0	129	P59374	pseudomonas	513	3	50.0	139	1	CO8E_RAT	P55314	rattus norv
441	1	RSF1_PSESM	129	3	50.0	129	Q889u8	pseudomonas	514	3	50.0	140	1	REL3_RAT	Q8bf83	rattus norv
442	1	VAF2_DROME	129	3	50.0	129	Q9vnl3	drosofila	515	3	50.0	140	1	YQIB_ECOLI	P36652	escherichia
443	1	DHSC_PARDE	130	3	50.0	130	Q59659	paracoccus	516	3	50.0	141	1	CH16_DROSO	P24511	drosofila
444	1	GLOV_HYACE	130	3	50.0	130	P81048	hyalophora	517	3	50.0	141	1	FABP_ANOGA	Q17017	anopheles g
445	1	LVIG_HUMAN	130	3	50.0	130	P06316	homo sapien	518	3	50.0	141	1	REL3_MOUSE	Q8chk2	mus musculu
446	1	MIA_MOUSE	130	3	50.0	130	Q61865	mus musculu	519	3	50.0	141	1	GLB1_LUCPE	P41260	lucina pect
447	1	NLR_DESGI	130	3	50.0	130	O50258	desulfovibr	520	3	50.0	142	1	NUSB_STRCO	Q9kx70	streptomyce
448	1	RR11_ODOSI	130	3	50.0	130	P49499	odontella s	521	3	50.0	142	1	NXT2_HUMAN	Q9npj8	homo sapien
449	1	RS11_SHEON	130	3	50.0	130	P59375	shewanella	522	3	50.0	142	1	OC17_CHICK	Q9pr88	gallus gall
450	1	RS11_SYNP6	130	3	50.0	130	O24709	synechococc	523	3	50.0	142	1	PTP_AC1JO	O52787	acinetobact
451	1	RS11_SYNY3	130	3	50.0	130	P73298	synechocyst	524	3	50.0	142	1	RPB6_SCHPO	P36595	schizosacch
452	1	RS11_XANCP	130	3	50.0	130	Q9z3e9	xanthomonas	525	3	50.0	142	1	U426_HSVMP	Q05104	marek's dis
453	1	TKN1_BOVIN	130	3	50.0	130	P01289	bos taurus	526	3	50.0	143	1	CRCB_XYLFA	Q9pde5	xylella fas
454	1	TKN1_MESAU	130	3	50.0	130	Q60541	mesocricetu	527	3	50.0	143	1	IL3_MAGMU	P25140	macaca mla
455	1	TKN1_MOUSE	130	3	50.0	130	P41539	mus musculu	528	3	50.0	143	1	FLAV_TRIER	O52659	trichodesmi
456	1	TKN1_RAT	130	3	50.0	130	P06767	rattus norv	529	3	50.0	144	1	GLB_APLJU	P14393	aplysia jul
457	1	UCR6_ECHMU	130	3	50.0	130	Q9gp40	echinococcu	530	3	50.0	144	1	GLB_APLJU	P02211	aplysia kur
458	1	Y056_MYCTU	130	3	50.0	130	P71953	mycobacteri	531	3	50.0	144	1	NUSB_HARIN	P45150	haemophilus
459	1	ABAI_TRIAB	131	3	50.0	131	P81111	trimeresuru	532	3	50.0	144	1	NUSB_STRAW	Q82774	streptomyce
460	1	ATPN_CAEEL	131	3	50.0	131	Q18803	caenorhabdi	533	3	50.0	144	1	RL15_SULAC	Q05643	sulfolobus
461	1	ATPO_CAEEL	131	3	50.0	131	P90921	caenorhabdi	534	3	50.0	144	1	RL15_SULSO	Q9ux85	sulfolobus
462	1	FRDC_PROVU	131	3	50.0	131	P20923	proteus vul	535	3	50.0	144	1	VMTT_LAMBD	P03735	bacterioph
463	1	OREX_HUMAN	131	3	50.0	131	O43612	homo sapien	536	3	50.0	144	1	YCD3_METFE	Q13583	bacterioph
464	1	OREX_PIG	131	3	50.0	131	O77668	sus scrofa	537	3	50.0	144	1	ENPP_BBP22	P93735	methanother
465	1	RPB6_DROME	131	3	50.0	131	Q24320	drosofila	538	3	50.0	145	1	ENPP_BBP22	Q13583	bacterioph
466	1	RS11_ANASP	131	3	50.0	131	Q9ypk2	anabena sp	539	3	50.0	145	1	GT22_D1ACA	Q03425	dianthus ca
467	1	RS11_NEISERIA	131	3	50.0	131	Q9jqr2	neisseria m	540	3	50.0	145	1	IAAA_HORVU	P28041	hordeum vul
468	1	ABBA_TRIAB	132	3	50.0	132	P81115	trimeresuru	541	3	50.0	145	1	LYC_OPHO	Q91159	opisthocomu
469	1	HEX9_ADE40	132	3	50.0	132	P48312	human adeno	542	3	50.0	145	1	NUIM_TRYBB	P30826	trypanosoma
470	1	MRKF_KLEPN	132	3	50.0	132	P21650	klebsiella	543	3	50.0	145	1	SYCN_MOUSE	Q8vc77	mus musculu
471	1	RS11_CHLCV	132	3	50.0	132	Q824n2	chlamydophi	544	3	50.0	145	1	SYCN_RAT	Q35775	rattus norv

545	3	50.0	145	1	VPRE_HUMAN	P12018 homo sapien	618	3	50.0	157	1	MMHA_AKGHA	O9Y9G9 agkistrodon
546	3	50.0	145	1	YAC1_METSO	P27096 methanohri	619	3	50.0	157	1	NDK_PYRO	O58439 pyrococcus
547	3	50.0	145	1	YCEA_PAEIA	P29718 paenibacilli	620	3	50.0	157	1	SSRP_BRAJA	Q5rh44 bradyrhizob
548	3	50.0	146	1	CYMS_RAT	P04166 rattus norv	621	3	50.0	157	1	UL51_HCNVA	P17692 human cytom
549	3	50.0	146	1	GLB_APLLI	P02210 aplysia lim	622	3	50.0	157	1	YIAM_ECOLI	P37674 escherichia
550	3	50.0	146	1	GLB_BURLI	P29287 burساتella	623	3	50.0	157	1	YWMA_BACSU	P70958 bacillus su
551	3	50.0	146	1	HV2I_HUMAN	P06331 homo sapien	624	3	50.0	158	1	CU14_HUMAN	P56557 homo sapien
552	3	50.0	146	1	IXB_TRIFL	P23807 trimeresura	625	3	50.0	158	1	CU14_MOUSE	O9dlx9 mus musculus
553	3	50.0	146	1	MMHB_AGRHA	Q9Y192 agkistrodon	626	3	50.0	158	1	GLBI_CHITH	P02221 chironomus
554	3	50.0	146	1	MOAE_RHOSH	Q53091 rhodobacter	627	3	50.0	158	1	RNKD_SAGOE	P47786 saguinus oe
555	3	50.0	147	1	CS19_HUMAN	Q9H491 homo sapien	628	3	50.0	159	1	CYPC_STRCO	P23154 streptomyce
556	3	50.0	147	1	G817_XENLA	P07733 xenopus lae	629	3	50.0	159	1	SSRP_RHILO	Q985B9 rhizobium l
557	3	50.0	147	1	Y565_METJA	Q57985 methanococ	630	3	50.0	159	1	YHA6_YEAST	P38751 saccharomyc
558	3	50.0	148	1	GLB3_TYLHE	P13578 tyloerhynch	631	3	50.0	160	1	GLB2_CHITH	P02222 chironomus
559	3	50.0	148	1	HUPG_BRAJA	P48339 bradyrhizob	632	3	50.0	160	1	GREB_VIBVU	Q8ddu7 vibrio vuln
560	3	50.0	148	1	LYC1_RAT	P00697 rattus norv	633	3	50.0	160	1	RRAI_VIBPA	Q878d2 vibrio para
561	3	50.0	148	1	LYCM_MOUSE	P08905 mus musculus	634	3	50.0	160	1	RRAI_VIBVU	Q8dep0 vibrio vuln
562	3	50.0	148	1	LYCP_MOUSE	P17897 mus musculus	635	3	50.0	160	1	RT2C_ACTPL	P15376 actinobacil
563	3	50.0	148	1	MYG_GALGA	P14397 galeorhinus	636	3	50.0	160	1	Y4FE_RHISN	P55443 rhizobium s
564	3	50.0	148	1	REGQ_BPAPS	Q8tlu3 bacterioph	637	3	50.0	160	1	YCDZ_SALTY	O54290 salmonella
565	3	50.0	148	1	RS19_EMENI	P27073 emericella	638	3	50.0	160	1	YFIB_ECOLI	P07021 escherichia
566	3	50.0	148	1	SSRP_NEIMA	Q51111 neisseria m	639	3	50.0	161	1	GLB9_CHITH	P02223 chironomus
567	3	50.0	148	1	UBCC_SCHPO	O13685 schizosacch	640	3	50.0	161	1	GREB_VIBCH	Q9kn17 vibrio chol
568	3	50.0	148	1	Y18K_MSVS	P14989 maize strea	641	3	50.0	161	1	HLB_TRETO	P07803 trema tomen
569	3	50.0	148	1	YF58_MYCTU	Q10772 mycobacteri	642	3	50.0	161	1	NDK_PYRFU	Q8u2a8 pyrococcus
570	3	50.0	148	1	YK83_YERPE	Q8zes0 yersinia pe	643	3	50.0	161	1	RRAI_VIBCH	Q8skp1 vibrio chol
571	3	50.0	148	1	YORX_PYRMO	P20298 pyrococcus	644	3	50.0	162	1	CVPA_ECOLI	P08550 escherichia
572	3	50.0	149	1	HUPG_RHILV	P28149 rhizobium l	645	3	50.0	162	1	HLB_HORVU	O42831 hordeum vul
573	3	50.0	149	1	NDK1_SACOF	P93554 saccharum o	646	3	50.0	162	1	IPYR_MYCLE	O69540 mycobacteri
574	3	50.0	149	1	YGAM_ECOLI	P76626 escherichia	647	3	50.0	162	1	IPYR_MYCTU	O69379 mycobacteri
575	3	50.0	150	1	NUPM_CABEL	Q18359 caenorhabdi	648	3	50.0	162	1	RECX_XANOR	O9ap31 xanthomonas
576	3	50.0	150	1	RI9E_TREAC	Q9hm21 thermoplasm	649	3	50.0	162	1	YPU1_RHOCA	P26157 rhodobacter
577	3	50.0	150	1	TCQP_VIBCH	P29490 vibrio chol	650	3	50.0	163	1	GLB2_CHITH	Q23761 chironomus
578	3	50.0	150	1	VHR2_CAMPS	Q8v228 camelopox vi	651	3	50.0	163	1	GLB2_CHITH	P29245 chironomus
579	3	50.0	150	1	VHR2_MONPV	Q8v566 monkeypox v	652	3	50.0	163	1	IPYR_STRCO	Q9x819 streptomyce
580	3	50.0	150	1	VHR2_VACCV	P17363 vaccinia vi	653	3	50.0	163	1	PUR6_PSEAE	P72157 pseudomonas
581	3	50.0	150	1	VHR2_VARV	P33860 variola vir	654	3	50.0	163	1	YCDZ_ECOLI	P75916 escherichia
582	3	50.0	151	1	CT78_HUMAN	Q9br46 homo sapien	655	3	50.0	164	1	PR12_HORVU	P35792 hordeum vul
583	3	50.0	151	1	LE14_GOSHI	P46518 gossypium h	656	3	50.0	164	1	PR13_HORVU	P35793 hordeum vul
584	3	50.0	151	1	Y4JR_RHISN	P55518 rhizobium s	657	3	50.0	164	1	PR1_HORVU	Q50968 hordeum vul
585	3	50.0	152	1	CYPC_STRCN	Q02572 streptomyce	658	3	50.0	164	1	YQJ3_CABEL	P34626 caenorhabdi
586	3	50.0	152	1	LE14_SOYBN	P46519 glycine max	659	3	50.0	165	1	CTE1_HUMAN	Q9nub4 homo sapien
587	3	50.0	152	1	LXKS_HELPJ	Q9zms8 helicobacte	660	3	50.0	165	1	HLB_MAIZE	Q9fy42 zea mays (m
588	3	50.0	152	1	LXKS_ARCFU	Q29457 archaeoglob	661	3	50.0	165	1	HLB_ZEAMP	Q9m593 zea mays (s
589	3	50.0	152	1	TNCP_PATYE	P35622 patinopecte	662	3	50.0	165	1	LITH_MOUSE	P43137 mus musculus
590	3	50.0	153	1	ENPP_BP21	P27358 bacterioph	663	3	50.0	165	1	LITH_RAT	P10758 rattus norv
591	3	50.0	153	1	ENPP_LAMBD	P00726 bacterioph	664	3	50.0	165	1	LKTC_PASSP	P53124 pasteurella
592	3	50.0	153	1	RECX_PSEAE	P37860 pseudomonas	665	3	50.0	165	1	YRHL_RHOSH	Q53229 rhodobacter
593	3	50.0	153	1	RS15_METJA	P54012 methanococ	666	3	50.0	166	1	HLB1_ORYSA	O04986 oryza sativ
594	3	50.0	153	1	R2PD_ECOLI	P75719 escherichia	667	3	50.0	166	1	PAL_PSEPK	P43036 pseudomonas
595	3	50.0	153	1	Y18K_MSVN	P14978 maize strea	668	3	50.0	166	1	RECX_SALTI	Q8z404 salmonella
596	3	50.0	153	1	YCGN_SALTI	Q8z682 salmonella	669	3	50.0	166	1	RECX_SALTY	Q8zmk5 salmonella
597	3	50.0	153	1	YCGN_SALTY	Q8z682 salmonella	670	3	50.0	167	1	HLB4_ORYSA	Q94f17 oryza sativ
598	3	50.0	154	1	AP16_YEAST	P40518 saccharomyc	671	3	50.0	167	1	LKCI_PASHA	P16533 pasteurella
599	3	50.0	154	1	CORZ_DROME	Q86377 drosophila	672	3	50.0	167	1	LKCB_PASHA	P55130 pasteurella
600	3	50.0	154	1	MER2_EUPOC	O15825 euplotes oc	673	3	50.0	167	1	LKCB_PASHA	P55131 pasteurella
601	3	50.0	154	1	Y451_SYNY3	P74676 synechocyst	674	3	50.0	167	1	VHR2_YABAM	Q9qb04 yaba monkey
602	3	50.0	154	1	YHAV_ECOLI	P42901 escherichia	675	3	50.0	168	1	LKTC_ACTAC	P1461 actinobacil
603	3	50.0	155	1	LXKS_HELPJ	O24931 helicobacte	676	3	50.0	168	1	PSA_DICDI	P12729 dictyosteli
604	3	50.0	155	1	MOAC_COREF	Q8fu35 corynebacte	677	3	50.0	168	1	VVH8_VIBVU	P19248 vibrio vuln
605	3	50.0	155	1	REB6_YEAST	P20435 saccharomyc	678	3	50.0	168	1	YCIE_ECOLI	P21363 escherichia
606	3	50.0	155	1	YC36_GUITH	O78501 guillardia	679	3	50.0	168	1	YI22_MYCTU	Y50706 mycobacteri
607	3	50.0	156	1	CDN2_HUMAN	P42771 homo sapien	680	3	50.0	169	1	CX41_THUOB	Q9180 thynnus obe
608	3	50.0	156	1	MOAC_COREG	Q8ntul corynebacte	681	3	50.0	169	1	HLB2_ORYSA	O04985 oryza sativ
609	3	50.0	156	1	NUKM_PARTE	P15602 paramecium	682	3	50.0	169	1	HLB3_ORYSA	Q94f68 oryza sativ
610	3	50.0	156	1	PN20_SCHPO	O14313 schizosacch	683	3	50.0	169	1	LFS_ALICE	P59082 allium cepa
611	3	50.0	156	1	SOXR_PSEAE	Q51506 pseudomonas	684	3	50.0	169	1	NAPE_ALCEU	P39186 alcaigenes
612	3	50.0	156	1	VPG_PLRV	P10471 potato leaf	685	3	50.0	169	1	RIMM_NEIMA	Q9jv49 neisseria m
613	3	50.0	156	1	VPG_PLRV1	P17524 potato leaf	686	3	50.0	169	1	RIMM_NEIMB	Q9K0K3 neisseria m
614	3	50.0	156	1	VPG_PLRV1	P17523 potato leaf	687	3	50.0	169	1	YIST_BACSU	O07939 bacillus su
615	3	50.0	156	1	VPG_PLRVW	P11625 potato leaf	688	3	50.0	170	1	HLCI_ECOLI	P09984 escherichia
616	3	50.0	156	1	YU69_MYCTU	P17665 mycobacteri	689	3	50.0	170	1	HLYC_ECOLI	P06736 escherichia
617	3	50.0	157	1	GLB1_PARCH	P15161 paracaudina	690	3	50.0	170	1	VEAF_HCNVA	P09694 human cytom

691	3	50.0	171	1	HUNB_SCRAAL	O46254 scaptomyza	764	3	50.0	187	1	NIP3_MOUSE	O55003 mus musculus
692	3	50.0	171	1	PUR6_MYCLE	P46702 mycobacteri	765	3	50.0	187	1	VA22_VARV	P33845 variola vir
693	3	50.0	172	1	CX42_RAT	Q91y94 rattus norv	766	3	50.0	187	1	YK06_AERPE	Q9vad3 aeropyrum p
694	3	50.0	172	1	MEAL1_HUMAN	Q16626 homo sapien	767	3	50.0	188	1	INL6_RAT	Q9wv41 rattus norv
695	3	50.0	172	1	RT1C_ACTPL	P55132 actinobacil	768	3	50.0	188	1	RL5_FYRAB	Q9vlu9 pyrococcus
696	3	50.0	172	1	UL45_HSV11	P10229 herpes simp	769	3	50.0	188	1	RL5_FYRAB	Q59431 pyrococcus
697	3	50.0	172	1	UL45_HSV1K	P28987 herpes simp	770	3	50.0	188	1	SPR_ECOLI	P77685 escherichia
698	3	50.0	172	1	UL45_HSV1M	P06482 herpes simp	771	3	50.0	188	1	UBCB_YEAST	P52491 saccharomyc
699	3	50.0	172	1	Y856_PYRHO	O58586 pyrococcus	772	3	50.0	189	1	BBP_FIBER	Q94644 pieris bras
700	3	50.0	172	1	YC46_PYRAB	Q9uza8 pyrococcus	773	3	50.0	189	1	NC51_YEAST	Q06389 saccharomyc
701	3	50.0	173	1	CLF8_HUMAN	Q8izv2 homo sapien	774	3	50.0	189	1	Y064_METJA	Q80376 methanococc
702	3	50.0	173	1	CLF8_MOUSE	Q9czr4 mus musculu	775	3	50.0	189	1	YMFJ_ECOLI	P75976 escherichia
703	3	50.0	173	1	FLAV_HAEIN	P44562 haemophilus	776	3	50.0	189	1	YWOL_BACSU	P34573 bacillus su
704	3	50.0	173	1	LIT2_MOUSE	Q08731 mus musculu	777	3	50.0	190	1	PHB2_HUMAN	Q9ue74 homo sapien
705	3	50.0	173	1	NU6M_SCVCA	O79412 scyllorhinu	778	3	50.0	190	1	VE03_VACCC	P21081 vaccinia vi
706	3	50.0	173	1	NU6M_SQUAC	Q92443 squalus aca	779	3	50.0	190	1	VE03_VACCV	P21605 vaccinia vi
707	3	50.0	173	1	NUDH_RHILLO	Q98f04 rhizobium l	780	3	50.0	190	1	VE03_VARV	P33863 variola vir
708	3	50.0	173	1	RT3C_ACTPL	Q04474 actinobacil	781	3	50.0	191	1	INL6_MOUSE	Q9y905 mus musculu
709	3	50.0	173	1	Y013_BHPH1	P51715 bacterioph	782	3	50.0	191	1	TH11_MOUSE	Q9dca2 mus musculu
710	3	50.0	174	1	HLC2_ECOLI	P09985 escherichia	783	3	50.0	191	1	TH1F_MBSER	O81332 mesembryant
711	3	50.0	174	1	MEAL1_BOVIN	Q29407 bos taurus	784	3	50.0	191	1	TXLA_SYNP7	P35088 synechooccc
712	3	50.0	174	1	MEAL1_MOUSE	Q54327 mus musculu	785	3	50.0	191	1	YAED_ECOLI	P31546 escherichia
713	3	50.0	174	1	NUOB_RICPR	Q9zdh2 rickettsia	786	3	50.0	192	1	KITH_VIBCH	Q9ksr9 vibrio chol
714	3	50.0	174	1	PADC_VIBCH	Q9kpx2 vibrio chol	787	3	50.0	192	1	KITH_VIBPA	Q87qj8 vibrio para
715	3	50.0	174	1	PYRR_RALSO	Q9y113 raietonia s	788	3	50.0	192	1	KITH_VIBVU	Q8d832 vibrio vuln
716	3	50.0	175	1	CT38_HUMAN	Q9nuv7 homo sapien	789	3	50.0	192	1	MOBA_NEIMA	P58747 neisseria m
717	3	50.0	175	1	DIAC_BOVIN	Q01458 bos taurus	790	3	50.0	192	1	MOBA_NEIMB	P58747 neisseria m
718	3	50.0	175	1	FLAV_SHIFL	Q83880 ehigella fl	791	3	50.0	192	1	RR4B_CVACA	O22029 cyanidium c
719	3	50.0	175	1	NUGC_ANASP	Q44241 anabaena sp	792	3	50.0	193	1	BCLW_MOUSE	Q92843 homo sapien
720	3	50.0	175	1	NUGC_ANAVA	Q9xb16 anabaena va	793	3	50.0	193	1	BCLW_MOUSE	P70345 mus musculu
721	3	50.0	176	1	C552_PARDE	P54820 paracoccus	794	3	50.0	193	1	DEF2_CORBF	Q8fmd0 corynebacte
722	3	50.0	176	1	VA22_VACCC	P20997 vaccinia vi	795	3	50.0	193	1	TSAL_MOUSE	Q9f916 mus musculu
723	3	50.0	177	1	CRAB_SQUAC	P02512 squalus aca	796	3	50.0	193	1	YBF9_YEAST	P34224 saccharomyc
724	3	50.0	177	1	OM19_BRUME	Q44663 brucella me	797	3	50.0	194	1	COX2_PARDE	P08303 paracoccus
725	3	50.0	177	1	Y086_METWA	Q8q0q0 methanosarc	798	3	50.0	194	1	MOBA_SYNP7	O06866 synechooccc
726	3	50.0	177	1	YH86_CIFPU	O28488 archaeoglob	799	3	50.0	194	1	NIP3_HUMAN	Q12993 homo sapien
727	3	50.0	178	1	DSBB_VIBPA	Q87n03 vibrio para	800	3	50.0	195	1	AAC2_MYCFO	Q49157 mycobacteri
728	3	50.0	178	1	VHR2_YLDV	Q9dhp6 yaba-like d	801	3	50.0	195	1	FOS_SHEEP	O02761 ovis aries
729	3	50.0	179	1	CAS2_RAT	P02667 rattus norv	802	3	50.0	195	1	YFIK_ECOLI	P38101 escherichia
730	3	50.0	179	1	NUGC_SYNV3	P19125 synechocyst	803	3	50.0	196	1	NODA_MESPL	Q8vvh1 mesorhizobi
731	3	50.0	179	1	PYRE_MYCTU	O53717 mycobacteri	804	3	50.0	196	1	NODA_MESS7	Q8vvh1 mesorhizobi
732	3	50.0	179	1	YGJP_ECOLI	P42597 escherichia	805	3	50.0	196	1	NODA_RHIGA	P50348 rhizobium g
733	3	50.0	180	1	CYSH_RHTR	Q33579 rhizobium t	806	3	50.0	196	1	NODA_RHILT	P04673 rhizobium l
734	3	50.0	180	1	ISFZ_YERPE	Q9zeh5 yersinia pe	807	3	50.0	196	1	NODA_RHIME	P02962 rhizobium m
735	3	50.0	180	1	TXLA_SYNV3	P73920 synechocyst	808	3	50.0	196	1	NODA_RHISN	P50349 rhizobium s
736	3	50.0	180	1	Y554_HAEIN	P44014 haemophilus	809	3	50.0	196	1	NODA_RHITR	O53252 rhizobium t
737	3	50.0	180	1	YC55_PYRHO	O58998 pyrococcus	810	3	50.0	196	1	NODA_SINTE	Q8vvf0 sinorhizobi
738	3	50.0	180	1	YW60_XANCP	Q59586 xanthomonas	811	3	50.0	196	1	RS7_AERPE	Q9yau8 aeropyrum p
739	3	50.0	180	1	YW06_XANAC	Q8ph54 xanthomonas	812	3	50.0	196	1	YJAG_HAEIN	F44709 haemophilus
740	3	50.0	181	1	AAC2_MYCTU	P95219 mycobacteri	813	3	50.0	196	1	YM87_CORGL	Q8nnb7 corynebacte
741	3	50.0	181	1	CHMU_ERWHE	P42517 erwinia her	814	3	50.0	197	1	COAE_BACSU	O34932 bacillus su
742	3	50.0	181	1	PANC_ECOLI	P18103 escherichia	815	3	50.0	197	1	COP9_ARATH	P43255 arabidopsis
743	3	50.0	181	1	TRBB_ECOLI	P18035 escherichia	816	3	50.0	197	1	NODA_RHILLO	O52839 rhizobium l
744	3	50.0	181	1	Y06E_BPT4	P13311 bacterioph	817	3	50.0	197	1	NUOC_NEIMA	Q9jx80 neisseria m
745	3	50.0	181	1	YV17_METAC	Q8tlc0 methanosarc	818	3	50.0	197	1	NUOC_NEIMB	Q9k1c1 neisseria m
746	3	50.0	182	1	YNJA_ECOLI	P76222 escherichia	819	3	50.0	197	1	TMRB_BACSU	P12921 bacillus su
747	3	50.0	183	1	FLIZ_ECOLI	P52627 escherichia	820	3	50.0	197	1	YL52_HSVF4	Q00040 equine herp
748	3	50.0	183	1	IPYR_MYCFU	Q98q96 mycoplasma	821	3	50.0	197	1	YK45_YEAST	P36147 saccharomyc
749	3	50.0	183	1	VG71_BPML5	Q05286 mycobacteri	822	3	50.0	197	1	YRPA_SYNPZ	Q02426 synechooccc
750	3	50.0	184	1	PYRE_CORGL	Q8nm11 corynebacte	823	3	50.0	198	1	COX2_NOTPE	O03892 nothoprocta
751	3	50.0	184	1	YAEED_HAEIN	P46452 haemophilus	824	3	50.0	198	1	COX2_TINMA	O03895 tinamus maj
752	3	50.0	184	1	YC17_DROME	Q9vth95 drosophila	825	3	50.0	198	1	OPNR_AGRRH	P27872 agrobacteri
753	3	50.0	185	1	CVAC_BORPE	O45359 bordetella	826	3	50.0	198	1	PGD2_CHICK	O73888 gallus gall
754	3	50.0	185	1	END4_BPT4	P39250 bacterioph	827	3	50.0	198	1	PGD2_HUMAN	O60760 homo sapien
755	3	50.0	185	1	LYCV_BPPI	Q37875 bacterioph	828	3	50.0	198	1	PGD2_MOUSE	O9jhef7 mus musculu
756	3	50.0	186	1	MAUE_PARVE	Q56460 paracoccus	829	3	50.0	198	1	PGD2_RAT	C35543 rattus norv
757	3	50.0	186	1	RL18_HALMA	P14123 haloarcula	830	3	50.0	198	1	WH23_SFVKA	Q9q907 shope fibro
758	3	50.0	186	1	VNA2_TRTV	P33494 turkey rhin	831	3	50.0	198	1	YJV7_YEAST	P40893 saccharomyc
759	3	50.0	186	1	YJ89_MYCTU	Q10869 mycobactia	832	3	50.0	198	1	YR71_ECOLI	P21323 escherichia
760	3	50.0	187	1	ABP1_TOBAC	P33490 nicotiana t	833	3	50.0	199	1	CD69_MOUSE	P37217 mus musculu
761	3	50.0	187	1	ABP2_TOBAC	P33491 nicotiana t	834	3	50.0	199	1	COX2_APTAU	O03889 apteryx aus
762	3	50.0	187	1	AMPD_ENTCL	P82973 enterobacte	835	3	50.0	199	1	COX2_CASBE	O03890 casarius b
763	3	50.0	187	1	NDKM_HUMAN	O00746 homo sapien	836	3	50.0	199	1	COX2_DRONO	O03891 dromaeus no

764	3	50.0	187	1	NTP3_MOUSE	O55003 mus musculus
765	3	50.0	187	1	VA22_VARV	P33845 variola virus
766	3	50.0	187	1	YK06_AERPE	Q9vad3 aeropyrum pernix
767	3	50.0	188	1	INL6_RAT	Q9wv41 rattus norvegicus
768	3	50.0	188	1	RL5_FYRAB	Q9vlu9 pyrococcus
769	3	50.0	188	1	RL5_FYRHO	O59431 pyrococcus
770	3	50.0	188	1	SPR_ECOLI	P77685 escherichia
771	3	50.0	188	1	UBCB_YEAST	P52491 saccharomyces
772	3	50.0	189	1	BBP_FIBER	Q94644 pieris brassicae
773	3	50.0	189	1	NC51_YEAST	Q06389 saccharomyces
774	3	50.0	189	1	Y064_METJA	Q80376 methanococcus
775	3	50.0	189	1	YMFJ_ECOLI	P75976 escherichia
776	3	50.0	189	1	YWOC_BACSU	P34573 bacillus subtilis
777	3	50.0	190	1	PHB2_HUMAN	Q9ue74 homo sapiens
778	3	50.0	190	1	VE03_VACCC	P21081 vaccinia virus
779	3	50.0	190	1	VE03_VACCV	P21605 vaccinia virus
780	3	50.0	190	1	VE03_VARV	P33863 variola virus
781	3	50.0	191	1	INL6_MOUSE	Q9y905 mus musculus
782	3	50.0	191	1	RT11_MOUSE	Q9dca2 mus musculus
783	3	50.0	191	1	TH1F_MESCR	O81332 mesembryant
784	3	50.0	191	1	TXLA_SYNP7	P35088 synechococcus
785	3	50.0	191	1	YAED_ECOLI	P31546 escherichia
786	3	50.0	192	1	KITH_VIBCH	Q9kst9 vibrio cholerae
787	3	50.0	192	1	KITH_VIBPA	Q87qj8 vibrio parahaemolyticus
788	3	50.0	192	1	KITH_VIBVU	Q8d8r2 vibrio vulnificus
789	3	50.0	192	1	MOBA_NEIMA	Q9tuae5 neisseria meningitidis
790	3	50.0	192	1	MOBA_NEIMB	P58747 neisseria meningitidis
791	3	50.0	192	1	R4B4_CYACA	O22029 cyanidium ochroleucum
792	3	50.0	193	1	BCLW_HUMAN	Q28243 homo sapiens
793	3	50.0	193	1	BCLW_MOUSE	P70345 mus musculus
794	3	50.0	193	1	DEF2_COREF	Q8fmd0 corynebacterium
795	3	50.0	193	1	TSA1_MOUSE	Q9d9t6 mus musculus
796	3	50.0	193	1	YB99_YEAST	P34224 saccharomyc
797	3	50.0	194	1	COX2_PARDE	P08303 paracoccus
798	3	50.0	194	1	MOBA_SYNP7	O08866 synechococcus
799	3	50.0	194	1	NIP3_HUMAN	Q12983 homo sapiens
800	3	50.0	195	1	AA02_MYCFO	Q49157 mycobacterium
801	3	50.0	195	1	F05_SHEEP	O02761 ovis aries
802	3	50.0	195	1	YFIK_ECOLI	P38101 escherichia
803	3	50.0	196	1	NODA_MESPL	Q8vvh1 mesorhizobium
804	3	50.0	196	1	NODA_MESS7	Q9ran9 mesorhizobium
805	3	50.0	196	1	NODA_RHIGA	P50348 rhizobium g
806	3	50.0	196	1	NODA_RHILT	P04673 rhizobium l
807	3	50.0	196	1	NODA_RHIME	P20962 rhizobium m
808	3	50.0	196	1	NODA_RHISN	P50349 rhizobium s
809	3	50.0	196	1	NODA_RHITR	Q53252 rhizobium t
810	3	50.0	196	1	NODA_SINTE	Q8vvf0 sinorhizobium
811	3	50.0	196	1	R57_AERPE	Q9yau8 aeropyrum p
812	3	50.0	196	1	YIAG_HAEIN	P44709 haemophilus
813	3	50.0	196	1	YH87_CORGL	Q8nmb7 corynebacter
814	3	50.0	197	1	COAE_BACSU	O34932 bacillus su
815	3	50.0	197	1	COPE_ARATH	P43255 arabidopsis
816	3	50.0	197	1	NODA_RHILO	Q52839 rhizobium l
817	3	50.0	197	1	NUOC_NEIMA	Q9jx80 neisseria m
818	3	50.0	197	1	NUOC_NEIMB	O9k1c1 neisseria m
819	3	50.0	197	1	THRB_BACSU	P12921 bacillus su
820	3	50.0	197	1	UL52_HSV4	Q00040 equine herp
821	3	50.0	197	1	YK45_YEAST	P36147 saccharomyc
822	3	50.0	197	1	YKPA_SYNPZ	Q02426 synechococc
823	3	50.0	198	1	COX2_NOTPE	O03892 nothoproc
824	3	50.0	198	1	COX2_TINNA	O03895 tinamus maj
825	3	50.0	198	1	OPNR_AGRRH	P27872 agrobacteri
826	3	50.0	198	1	PGD2_CHICK	O73888 gallus gall
827	3	50.0	198	1	PGD2_HUMAN	O60760 homo sapien
828	3	50.0	198	1	PGD2_MOUSE	Q9jh7f mus musculu
829	3	50.0	198	1	PGD2_RAT	O35543 rattus norv
830	3	50.0	198	1	VH23_SFVKA	Q9c907 Shope fibro
831	3	50.0	198	1	XJV7_YEAST	P40893 saccharomyc
832	3	50.0	198	1	YR71_ECOLI	P21323 escherichia
833	3	50.0	199	1	C069_MOUSE	P37217 mus musculu
834	3	50.0	199	1	COX2_APTAU	O03889 apteryx aus
835	3	50.0	199	1	COX2_CASBE	O03890 casuarus b
836	3	50.0	199	1	COX2_DRONO	O03891 dromaius no

837	3	50.0	199	1	COX2_RHEAM	O03893	rhea.americ	910	3	50.0	211	1	NDK5_MOUSE	Q99mh5	mus.musculus
838	3	50.0	199	1	NHAA_PSECL	P27764	pseudomonas	911	3	50.0	211	1	THIE_ECOL5	Q8x6y0	escherichia
839	3	50.0	199	1	RS4_MYCPU	P99pk6	mycoplasma	912	3	50.0	211	1	THIE_ECOL6	Q8fb78	escherichia
840	3	50.0	199	1	R58_YEAST	P05754	saccharomyc	913	3	50.0	211	1	THIE_ECOLI	P03137	escherichia
841	3	50.0	199	1	Y266_HAEIN	P44603	haemophilus	914	3	50.0	211	1	THIE_SALTI	Q82325	salmonella
842	3	50.0	199	1	Y269_SYNY3	P73888	synechocyst	915	3	50.0	211	1	THIE_SALTY	Q91918	salmonella
843	3	50.0	199	1	Y874_HABIN	P73888	synechocyst	916	3	50.0	211	1	TRPF_PSEAE	Q59649	pseudomonas
844	3	50.0	200	1	NUPL_XENLA	P05221	haemophilus	917	3	50.0	211	1	TX10_HUMAN	O75333	homo.sapien
845	3	50.0	200	1	VATE_BORBU	O51123	xenopus.lae	918	3	50.0	211	1	YNQ8_CABEL	Q31984	caenorhabdi
846	3	50.0	200	1	YL86_COREF	Q8fnf8	corynebacte	919	3	50.0	211	1	ZFP5_ARATH	Q39264	arabidopsai
847	3	50.0	201	1	ABP1_MAIZE	P13689	zea.mays.(m	920	3	50.0	212	1	GRPE_LEPIN	O51868	leptospira
848	3	50.0	201	1	HAM1_LACIA	Q9c929	lactococcus	921	3	50.0	212	1	KTHY_SYNY3	O55933	synechocyst
849	3	50.0	201	1	NUCL_RHIME	O68854	rhizobium.m	922	3	50.0	212	1	NDK5_HUMAN	P56597	homo.sapien
850	3	50.0	201	1	OM25_BRUOV	Q45335	brucella.ov	923	3	50.0	212	1	PPIC_HUMAN	P45877	homo.sapien
851	3	50.0	201	1	UUC0_HCMVA	P16740	human.cytom	924	3	50.0	212	1	PPYL_HALN1	Q9h816	halobacteri
852	3	50.0	201	1	YPA2_LEGNE	P26881	legionella	925	3	50.0	212	1	TAL_BACSU	P19669	bacillus.su
853	3	50.0	202	1	COAE_CHLMU	Q9pjp9	chlamydia.m	926	3	50.0	212	1	US01_HCMVA	P09714	human.cytom
854	3	50.0	202	1	COAE_CHLTC	O84499	chlamydia.t	927	3	50.0	213	1	CPCF_SYNEL	P50038	synechococc
855	3	50.0	202	1	LEXA_ERWCA	O04596	erwinia.car	928	3	50.0	213	1	HIS1_BACSU	O34520	bacillus.su
856	3	50.0	202	1	NORE_PSEAE	Q9h210	pseudomonas	929	3	50.0	213	1	OM25_BRUAB	O44684	brucella.ab
857	3	50.0	202	1	RNFG_PASMO	Q9cnp4	pasteurella	930	3	50.0	213	1	OM25_BRUCA	O45110	brucella.ca
858	3	50.0	202	1	YJ72_YEAST	P47142	saccharomyc	931	3	50.0	213	1	OM25_BRUME	Q45321	brucella.me
859	3	50.0	203	1	CLDM_HUMAN	Q8n7p3	homo.sapien	932	3	50.0	213	1	OM25_BRUNE	O45326	brucella.ne
860	3	50.0	203	1	FMS5_ECOLI	P33781	escherichia	933	3	50.0	213	1	OM25_BRUSU	O45689	brucella.su
861	3	50.0	203	1	GTS_OMSL	P46088	onastrephe	934	3	50.0	213	1	PNCA_ECOLI	P21369	escherichia
862	3	50.0	203	1	PLY2_METAC	P58863	methanosarc	935	3	50.0	213	1	STR5_MOUSE	Q9epg7	mus.musculus
863	3	50.0	203	1	RR22_HUMAN	Q92737	homo.sapien	936	3	50.0	213	1	TRMB_SYNEL	Q8dh6	synechococc
864	3	50.0	204	1	ABP4_MAIZE	P33488	zea.mays.(m	937	3	50.0	213	1	TRPF_ACTICA	P16923	acinetobact
865	3	50.0	204	1	BACR_HALHM	P33969	halobacteri	938	3	50.0	213	1	VE4_HPV65	Q07873	human.papil
866	3	50.0	204	1	FHS2_SCHPO	Q9p7w2	schizosacch	939	3	50.0	214	1	ATPE_ALBCO	P48893	albinaria.c
867	3	50.0	204	1	HIS2_YERPE	Q8zfyl	yersinia.pe	940	3	50.0	214	1	GALLI_CANMA	P56539	candida.mal
868	3	50.0	204	1	NU6M_CHOCR	P48924	chondrus.cr	941	3	50.0	214	1	NODA_METNO	Q9f0c9	methylobact
869	3	50.0	204	1	SC7_SCHCO	P35794	schizophyll	942	3	50.0	214	1	NODE_RHIGA	P50354	rhizobium.g
870	3	50.0	204	1	SLI2_RALSO	O30920	raistonia.s	943	3	50.0	214	1	PPCT_HUMAN	O9uk16	homo.sapien
871	3	50.0	204	1	THIE_RHJET	O34294	rhizobium.e	944	3	50.0	214	1	PPCT_MOUSE	P53808	mus.musculus
872	3	50.0	204	1	UNG_HSVBC	P53764	bovine.herp	945	3	50.0	214	1	PPCT_RAT	P53809	rattus.norv
873	3	50.0	204	1	VT16_CABEL	Q10919	caenorhabdi	946	3	50.0	214	1	RLI_METKA	O8txs1	methanopyru
874	3	50.0	205	1	CNTA_SCHPO	Q9uu17	schizosacch	947	3	50.0	214	1	SC14_SCHCO	P35795	schizophyll
875	3	50.0	205	1	RNH2_CHLTE	Q8kaa5	chlorobium	948	3	50.0	214	1	TALI_LISIN	O927a3	listeria.in
876	3	50.0	205	1	TRPF_THEMEA	Q56320	thermotoga	949	3	50.0	214	1	TALI_LISMO	O8y3t8	listeria.mo
877	3	50.0	206	1	BACH_HALHM	P33970	halobacteri	950	3	50.0	214	1	ULD0_HCMVA	P16772	human.cytom
878	3	50.0	206	1	EPA4_MOUSE	O08542	mus.musculus	951	3	50.0	214	1	Y117_MYCGE	P47363	mycoplasma
879	3	50.0	206	1	GSPJ_ERWCH	P24689	erwinia.chr	952	3	50.0	215	1	CCME_PARDE	P52219	paracoccus
880	3	50.0	206	1	RNH2_METTH	O27102	methanobact	953	3	50.0	215	1	HIS5_STRAW	Q82aa2	streptomyce
881	3	50.0	206	1	TPIS_AEDTO	P92119	aedes.togoi	954	3	50.0	215	1	IF4E_APLCA	O7210	aphysia.cal
882	3	50.0	206	1	TPIS_ANOME	P91895	anopheles.m	955	3	50.0	215	1	NODE_RHLIT	P04676	rhizobium.1
883	3	50.0	206	1	TPIS_CULPI	P91919	culicx.pipie	956	3	50.0	215	1	NODE_RHISN	P50355	rhizobium.s
884	3	50.0	206	1	TRPF_PSEPK	Q88le0	pseudomonas	957	3	50.0	215	1	PTH_DEIRA	O9rrw3	deinococcus
885	3	50.0	206	1	UREG_UREPA	Q56561	ureaplasma	958	3	50.0	215	1	SFT2_YEAST	P38166	saccharomyc
886	3	50.0	206	1	Y930_HAEIN	P44077	haemophilus	959	3	50.0	215	1	Y034_NPVAC	P21287	autographa
887	3	50.0	206	1	YGZC_YEAST	P53058	saccharomyc	960	3	50.0	215	1	Y233_XYLFA	O9pgr5	xyella.fas
888	3	50.0	207	1	LEXA_AERRY	Q44069	aeromonas.h	961	3	50.0	215	1	Y267_BUCAI	P57355	buchnera.ap
889	3	50.0	208	1	PSD_METAC	Q8tuf2	methanosarc	962	3	50.0	216	1	COX2_CALGO	P50661	callimico.g
890	3	50.0	208	1	RS8_CABEL	P48156	caenorhabdi	963	3	50.0	216	1	CSGD_ECOLI	P52106	escherichia
891	3	50.0	208	1	TESA_ECOLI	P29679	escherichia	964	3	50.0	216	1	CSGD_SALTY	O54294	salmonella
892	3	50.0	208	1	Y755_HALN1	Q9hrc8	halobacteri	965	3	50.0	216	1	DEF4_STRCO	Q9k4a0	streptomyce
893	3	50.0	208	1	YK69_CABEL	P34347	caenorhabdi	966	3	50.0	216	1	INAA_ECOLI	P27294	escherichia
894	3	50.0	209	1	CCX1_HUMAN	O15255	homo.sapien	967	3	50.0	216	1	KPT2_ARCFU	O28719	archaeoglob
895	3	50.0	209	1	RS3_THEMEA	P46772	thermotoga	968	3	50.0	216	1	NODB_RHILV	P04339	rhizobium.1
896	3	50.0	209	1	ULB8_HCMVA	P16834	human.cytom	969	3	50.0	216	1	PGSA_TREPA	O66076	treponema.p
897	3	50.0	210	1	ENGB_PSEPK	Q88rk5	pseudomonas	970	3	50.0	216	1	PIM1_ARCFU	O30199	archaeoglob
898	3	50.0	210	1	FTSQ_AGRTU	O30990	agrobacteri	971	3	50.0	216	1	RGSU_MOUSE	Q9c8x4	mus.musculus
899	3	50.0	210	1	NIP3_CABEL	Q09969	caenorhabdi	972	3	50.0	216	1	RGSU_RAT	O70521	rattus.norv
900	3	50.0	210	1	NODA_BRAEL	P50326	bradyrhizob	973	3	50.0	216	1	SGAH_ECOLI	P39304	escherichia
901	3	50.0	210	1	NODA_BRAJA	Q9am20	bradyrhizob	974	3	50.0	216	1	Y192_XYLFT	Q87ev6	xyella.fas
902	3	50.0	210	1	NODA_BRASN	P50347	bradyrhizob	975	3	50.0	216	1	Y458_METJA	O57900	methanococc
903	3	50.0	210	1	NODA_BRASP	P04674	bradyrhizob	976	3	50.0	217	1	FLAI_METJA	Q58301	methanococc
904	3	50.0	210	1	RGSH_CHICK	Q9pwa0	gallus.gall	977	3	50.0	217	1	NODB_RHIME	P02963	rhizobium.m
905	3	50.0	210	1	XYNA_BACST	P45705	bacillus.st	978	3	50.0	217	1	O2A5_HUMAN	Q96x48	homo.sapien
906	3	50.0	210	1	YAC9_MAIZE	P03936	zea.mays.(m	979	3	50.0	217	1	RGSU_HUMAN	P49795	homo.sapien
907	3	50.0	210	1	Y043_HALN1	Q9hmb2	halobacteri	980	3	50.0	217	1	TAL_BRUME	Q8y142	brucella.me
908	3	50.0	210	1	YQS3_CABEL	Q09311	caenorhabdi	981	3	50.0	217	1	TAL_BRUSU	Q8fyq9	brucella.su
909	3	50.0	210	1	YRBL_ECOLI	P46021	escherichia	982	3	50.0	217	1	TRPF_CANGA	P50857	candida.gla

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983 3 50.0 217 1 UNG_PSEDE
984 3 50.0 217 1 UNG_STR3
985 3 50.0 217 1 UNG_STRMU
986 3 50.0 217 1 UREF_SYNY3
987 3 50.0 218 1 A4GT_POMPY
988 3 50.0 218 1 KAD_BORPE
989 3 50.0 218 1 MOBA_AGR5
990 3 50.0 218 1 NIPL_MOUSE
991 3 50.0 218 1 RS5_AERPE
992 3 50.0 218 1 TAL_RHIL0
993 3 50.0 218 1 UL71_EBV
994 3 50.0 218 1 Y522_HAEIN
995 3 50.0 218 1 YBOF_SCHPO
996 3 50.0 219 1 CVB6_HETTR
997 3 50.0 219 1 END3_BACSU
998 3 50.0 219 1 GLNP_ECOLI
999 3 50.0 219 1 NIPL_HUMAN
1000 3 50.0 219 1 NODB_BRAEL

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ALIGNMENTS

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RESULT 1
NRAM_IADBU
ID_NRAM_IADBU STANDARD; PRT; 470 AA.
AC Q07570;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Burjatia/652/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
-----
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EMBL; L06572; AAA43365.1; -.
HSP; P06820; 2BAT.
InterPro; IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT FT

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FT ACT SITE 273 273 BY SIMILARITY.
FT ACT SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51989 MW; DIA6F07460F6F8AD CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 2
NRAM_IADCH
ID_NRAM_IADCH STANDARD; PRT; 470 AA.
AC Q07571;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A viruses.";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
-----
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EMBL; L06573; AAA43367.1; -.
HSP; P06820; 2BAT.
InterPro; IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
DOMAIN 39 88 HEAD OF NEURAMINIDASE.
FT FT
FT DOMAIN 89 470 HEAD OF NEURAMINIDASE.
FT ACT SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 169AB89FBE8006DC CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 453 ADMSW 457

RESULT 3
NRAM_IADH2 STANDARD; PRT; 470 AA.
AC Q07572;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11358;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
-----
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or send an email to license@isb-sib.ch).
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EMBL; L06574; AAA43372.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
DR TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52015 MW; E1C1D3B2C650B93C CRC64;
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Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSW 5
Db 453 ADMSW 457

RESULT 4
NRAM_IADM2 STANDARD; PRT; 470 AA.
AC Q07573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
-----
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or send an email to license@isb-sib.ch).
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EMBL; L06575; AAA43404.1; -.
DR HSSP; P06820; 2BAT.
DR InterPro; IPR001860; Glyco_hydro_34; 1.
DR Pfam; PF00064; neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
DR TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9F364C1F49 CRC64;
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Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 5
NRAM_IADU3 STANDARD; PRT; 470 AA.
AC Q07599;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Ukraine/1/63).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC
CC EMBL; L06576; AA16234.1; -.
CC HSP; P06820; ZBAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 37 ANCHOR (BY SIMILARITY).
FT DOMAIN 38 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 PROBABLE.
FT ACT_SITE 275 275 PROBABLE.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457

RESULT 7
NRAM_IAHGD STANDARD; PRT; 470 AA.
AC Q07574;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
CC spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; L06584; AAA43428.1; -.
CC HSP; P06820; ZBAT.
CC InterPro; IPR001860; Glyco_hydro_34.
CC Pfam; PF00064; neur; 1.
CC ProDom; PD000431; Glyco_hydro_34; 1.
CC Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 273 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 453 ADWSW 457
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Q07577;
 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Herring gull/DE/677/88).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=38964;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 RT viruses";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
 CC spike on the surface of the virion.
 CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L06585; AAA3368.1; -;
 DR HSP; P06820; 28AT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 Db 453 ADWSW 457
 RESULT 8
 NRAM IAHJI
 ID _NRAM IAHJI STANDARD; PRT; 470 AA.
 AC Q07578;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Equine/Jilllin/1/89).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses; Influenzavirus A.
 OX NCBI_TaxID=11401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93212520; PubMed=8460490;
 RA Saito T., Kawaoka Y., Webster R.G.;
 RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
 RT viruses";
 RL Virology 193:868-876(1993).
 CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
 CC chains of the host cell surface proteins and from the viral
 CC envelope. Such a reaction prevents self-aggregation and facilitate
 CC the mobility of the virus to and from the site of infection.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
 CC alpha-(2->8)-glycosidic linkages of terminal sialic residues in
 CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
 CC synthetic substrates.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
 CC spike on the surface of the virion.
 CC -1- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; L06579; AAA3374.1; -;
 DR HSP; P06820; 28AT.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; neur; 1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 DR HydroLase; Glycosidase; Glycoprotein; Transmembrane.
 FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
 FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
 FT ACT_SITE 273 275 BY SIMILARITY.
 FT ACT_SITE 275 275 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;
 Query Match 83.3%; Score 5; DB 1; Length 470;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 Db 453 ADWSW 457
 RESULT 9
 NRAM IAAAE
 ID _NRAM IAAAE STANDARD; PRT; 470 AA.
 AC Q07583;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuraminidase (EC 3.2.1.18).
 GN NA.
 OS Influenza A virus (strain A/Mallard/Edmonton/220/90).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;

Influenza A viruses; Influenzavirus A.
NCBI_TaxID=38965;
[1]
SEQUENCE FROM N.A.
MEDLINE=93212520; PubMed=8460490;
Saito T., Kawaoka Y., Webster R.G.;
"Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses";
Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

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or send an email to license@isb-sib.ch).

EMBL; L06586; AAA43369.1; -;
HSP: P06820; 2BAT.
InterPro: IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630C3E11F2765 CRC64;
Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred.No.11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 453 ADWSW 457
RESULT 10
ID NRAW_IATKL STANDARD; PRT; 470 AA.
AC Q07585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
viruses";
RL Virology 193:868-876(1993).
CC -!- FUNCTION: Removes the terminal sialic acid from carbohydrate side
chains of the host cell surface proteins and from the viral
envelope. Such a reaction prevents self-aggregation and facilitate
the mobility of the virus to and from the site of infection.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
alpha-(2->8)-glycosidic linkages of terminal sialic residues in
oligosaccharides, glycoproteins, glycolipids, colominic acid and
synthetic substrates.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Viral membrane. Forms a mushroom-shaped
spike on the surface of the virion.
CC -!- SIMILARITY: Belongs to family 34 of glycosyl hydrolases.

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EMBL; L06588; AAA43410.1; -;
HSP: P06820; 2BAT.
InterPro: IPR001860; Glyco_hydro_34.
Pfam; PF00064; neur; 1.
ProDom; PD000431; Glyco_hydro_34; 1.
KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 BY SIMILARITY.
FT ACT_SITE 275 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52352 MW; DE573742ABFFB6B CRC64;
Query Match 83.3%; Score 5; DB 1; Length 470;
Best Local Similarity 100.0%; Pred.No.11;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 453 ADWSW 457
RESULT 11
ID MRJ5_APIME STANDARD; PRT; 598 AA.
AC O97432;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).
GN MRJP5.
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=99373663; PubMed=10441680;
RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.;

"The family of major royal jelly proteins and its evolution.";
J. Mol. Evol. 49:290-297(1999).
- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS
FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE
LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG
LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE
HONEYBEE QUEEN.
- SUBCELLULAR LOCATION: Secreted.
- TISSUE SPECIFICITY: Hypopharyngeal glands of nurse honey bees.
- DEVELOPMENTAL STAGE: Produced by the cephalic glandular system of
the nurse honey bee.
- SIMILARITY: Belongs to the major royal jelly protein family.
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EMBL; AF004842; AAD01205.1; -
InterPro; IPR003534; RoyalJelly.
Pfam; PF03022; MEJP; 2
PRINTS; PR01366; ROYALJELLY.
Signal; Repeat; Glycoprotein.
FT SIGNAL 1 17
FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.
FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 324 324 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 598 AA; 70236 MW; 2C603C77E7ACDF63 CRC64;
Query Match 83.3%; Score 5; DB 1; Length 598;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 DWSWA 6
Db 113 DWSWA 117
RESULT 12
LCGB LEUME STANDARD; PRT; 31 AA.
AC P81052;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Bacteriocin leucocin B.
OS Leuconostoc mesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=1245;
RN [1]
RP SEQUENCE.
RC STRAIN=TA33a;
RX MEDLINE=98274743; PubMed=9611809;
RA Papathanasopoulos M.A., Dykes G.A., Revol-Junelles A.-M., Delfour A.,
von Holy A., Hastings J.W.;
RT "Sequence and structural relationships of leucocins A-, B- and
C-TA33a from Leuconostoc mesenteroides TA33a.";
RL Microbiology 144:1343-1348(1998).
CC - FUNCTION: Inhibits a wide spectrum of lactic acid bacteria.
KW Bacteriocin; Antibiotic.
SQ SEQUENCE 31 AA; 3466 MW; 7C8DD9C387D34D55 CRC64;
Query Match 66.7%; Score 4; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 3 WSWA 6

Db
Db 6 WSWA 9
RESULT 13
TXD3 PARLU STANDARD; PRT; 36 AA.
AC P83258;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-palutoxin IT3 (Delta-palut3).
OS Paracaelotes luctuosus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Amaurobiidae; Paracaelotes.
OX NCBI_TaxID=185217;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20428467; PubMed=10971590;
RA Corzo G., Escoubas P., Stankiewicz M., Pelhate M., Kristensen C.P.,
Nakajima T.;
RT "Isolation, synthesis and pharmacological characterization of
delta-palutoxins IT, novel insecticidal toxins from the spider
Paracaelotes luctuosus (Amaurobiidae).";
RL Eur. J. Biochem. 267:5783-5795(2000).
CC - FUNCTION: Potent activity against S.litura larvae.
CC - FUNCTION: Binds to sodium channels and inhibits the inactivation
of the activated channels. This toxin is active only on insects
(by similarity).
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Expressed by the venom gland.
CC - MASS SPECTROMETRY: MW=3926.2; METHOD=MALDI.
CC - SIMILARITY: Belongs to the mu-agatoxin family.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0019871; F:sodium channel inhibitor activity; IDA.
DR GO: GO:0015070; F:toxin activity; IDA.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
FT DISULFID 3 19 BY SIMILARITY.
FT DISULFID 10 24 BY SIMILARITY.
FT DISULFID 18 34 BY SIMILARITY.
FT DISULFID 26 32 BY SIMILARITY.
SQ SEQUENCE 36 AA; 3934 MW; 9CDFDAD043A19804 CRC64;
Query Match 66.7%; Score 4; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 ADWS 4
Db 11 ADWS 14
RESULT 14
TXD1 PARLU STANDARD; PRT; 37 AA.
AC P83256;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta-palutoxin IT1 (Delta-palut1).
OS Paracaelotes luctuosus (Spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Amaurobiidae; Paracaelotes.
OX NCBI_TaxID=185217;
RN [1]
RP SEQUENCE, SYNTHESIS, FUNCTION, DISULFIDE BONDS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=20428467; PubMed=10971590;
RA Corzo G., Escoubas P., Stankiewicz M., Pelhate M., Kristensen C.P.,
Nakajima T.;
RT "Isolation, synthesis and pharmacological characterization of
delta-palutoxins IT, novel insecticidal toxins from the spider

```

RT Paracaelotes luctuosus (Amaurobiidae).";
RL Eur. J. Biochem. 267:5783-5795(2000).
CC -1- FUNCTION: Potent activity against S.litura larvae.
CC -1- FUNCTION: Binds to sodium channels and inhibits the inactivation
CC of the activated channels. This toxin is active only on insects.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=4037.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the mu-agatoxin family.
DR PIR; A59401; A59401.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0019871; F:sodium channel inhibitor activity; IDA.
DR GO; GO:0015070; F:toxin activity; IDA.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Amidation;
KW Sodium channel inhibitor.
FT DISULFID 2 18
FT DISULFID 9 23
FT DISULFID 17 33
FT DISULFID 25 31
FT DISULFID 37 37
FT MOD RES 37 37
FT SEQUENCE 37 AA; 4046 MW; E019DABCC35BC11E CRC64;
SQ
Query Match 66.7%; Score 4; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 10 ADWS 13

RESULT 15
ACYP_MYCTU STANDARD; PRT; 93 AA.
AC P56543;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative acylphosphatase (EC 3.6.1.7) (Acylphosphate
DE Phosphorylase).
GN ACYP OR RV2922.1C OR MT2991 OR MTCY338.11BC OR MB2947C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Bacher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL J. Bacteriol. 184:5479-5490(2002).

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RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., MONSENPE C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
RN [4]
RP IDENTIFICATION.
RC SPECIES=M.tuberculosis;
RA Barroch A.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: An acyl phosphate + H(2)O = a fatty acid anion
CC + phosphate.
CC -1- SIMILARITY: Belongs to the acylphosphatase family.
CC
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CC
CC EMBL; Z74697; -; NOT ANNOTATED_CDS.
CC EMBL; A5007121; AAK47318.1; -.
CC EMBL; BX248344; CAD96634.1; -.
CC TIGR; MT2991; -.
CC Tuberculist; RV2922.1c; -.
CC InterPro; IPR001792; Acylphosphatase.
CC Pfam; PF00708; Acylphosphatase; 1.
CC ProDom; PD001884; Acylphosphatase; 1.
CC PROSITE; PS00150; ACYLPHOSPHATASE_1; 1.
CC PROSITE; PS00151; ACYLPHOSPHATASE_2; 1.
CC KW Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 93 AA; 10206 MW; 63A90ED2D780DDEB CRC64;

Query Match 66.7%; Score 4; DB 1; Length 93;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 78 ADWS 81

RESULT 16
Y451_BUCAP STANDARD; PRT; 114 AA.
AC Q8K998;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein BUSG451.
GN BUSG451.
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tanas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002)
CC -1- SIMILARITY: BELONGS TO THE DSCR/DSVC FAMILY. STRONG, TO
CC E.COLI YOCK OR H.INFLUENZAE H11371.
CC
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 CC -----

DR EMBL; AE014121; AAM67994.1; -;
 DR InterPro; IPR007453; DsrC.
 DR Pfam; PF04358; DsrC; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 114 AA; 13332 MW; 775C9CF21A9AB41A CRC64;

Query Match 66.7%; Score 4; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

Db 26 ADWS 29

RESULT 17

YRDN_BACSU STANDARD; PRT; 128 AA.
 AC P94502; O08187;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable tautomerase yrdN (EC 5.3.2.-).
 GN YRDN OR BSU26660.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / SMY;
 RC MEDLINE=97175526; PubMed=9023181;
 RA Belitsky B.R., Sonenshein A.L.;
 RA "Altered transcription activation specificity of a mutant form of
 RT Bacillus subtilis GltR, a LysR family member.";
 RL J. Bacteriol. 179:1035-1043(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=97453479; PubMed=9308178;
 RA Sorokin A., Bolotin A., Purnelle B., Hilbert H., Lauber J.,
 RA Dusterhoeft A., Ehrlich S.D.;
 RT "Sequence of the Bacillus subtilis genome region in the vicinity of
 RT the lev operon reveals two new extracytoplasmic function RNA
 RL polymerase sigma factors SigV and SigZ.";
 RL Microbiology 143:2939-2943(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RC MEDLINE=98044033; PubMed=9384377;
 RA Kunst P., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holbappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasehara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpetra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis";
 RL Nature 390:249-256(1997).
 CC -!- FUNCTION: PUTATIVE TARGET OF GLTR.
 CC -!- SIMILARITY: Belongs to the tautomerase family.
 CC -----

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DR EMBL; U79494; AAB47964.1; -;
 DR EMBL; U93876; AAB80906.1; -;
 DR EMBL; Z99117; CAB14607.1; -;
 DR PIR; E69973; E69973.
 DR Subtilist; BG12287; YrdN.
 DR InterPro; IPR004370; Taut.
 DR Pfam; PF01361; Tautomerase; 1.
 KW Isomerase; Complete proteome.
 FT INIT MET 0
 FT ACT SITE 1 1 CATALYTIC BASE (BY SIMILARITY).
 SQ SEQUENCE 128 AA; 14550 MW; 6D148A7184E720EF CRC64;

Query Match 66.7%; Score 4; DB 1; Length 128;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

Db 112 ADWS 115

RESULT 18

VG29_BPMD2 STANDARD; PRT; 147 AA.
 AC O64223;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Gene 29 protein (GP29).
 GN 29.
 OS Mycobacteriophage D29.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
 OX NCBI_TaxID=28369;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98300335; PubMed=9636706;
 RA Ford M.E., Sarkis G.J., Belanger A.E., Hendrix R.W., Hatfull G.F.;
 RT "Genome structure of mycobacteriophage D29: implications for phage
 RT evolution.";
 RL J. Mol. Biol. 279:143-164(1998).
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 CC -----

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CC -----
DR EMBL; AF022214; AAC18470.1; -.
DR PIR; C72803; C72803.
SQ SEQUENCE 147 AA; 16982 MW; 54B877CBEDA82C33 CRC64;

Query Match
Best Local Similarity 66.7%; Score 4; DB 1; Length 147;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 40 ADWS 43

RESULT 19
VG29 BPML5 STANDARD; PRT; 147 AA.
AC O05236.
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Gene 29 protein (GP29).
GN 29.
OS Mycobacteriophage L5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC L5-like viruses.
OX NCBI_TaxID=311757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -----
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CC -----
DR EMBL; Z18946; CAA79405.1; -.
DR PIR; S30974; S30974.
SQ SEQUENCE 147 AA; 16900 MW; 4DC675311403D3B9 CRC64;

Query Match
Best Local Similarity 66.7%; Score 4; DB 1; Length 147;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 40 ADWS 43

RESULT 20
YB19 PSEPK STANDARD; PRT; 160 AA.
AC Q88NT5;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0225 protein PP1119.
GN PP1119.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

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RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzes A.,
RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
LAuber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
Fraser C.M.;
RA "Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440.";
RT Environ. Microbiol. 4:799-808(2002)
RL -!- SIMILARITY: Belongs to the UPF0225 family.
CC -----
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CC -----
DR EMBL; AE016778; AAN66744.1; -.
DR TIGR; PPI119; -.
DR HAMAP; MF_00612; -.
DR InterPro; IPR004027; SEC_C_motif.
DR Pfam; PF02810; SEC-C; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 160 AA; 17414 MW; 1213A502E31732B6 CRC64;
SQ

Query Match
Best Local Similarity 66.7%; Score 4; DB 1; Length 160;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 68 ADWS 71

RESULT 21
CX41 MOUSE STANDARD; PRT; 169 AA.
ID -CX41 MOUSE
AC P19783;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor
DE (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV).
DE COX4I1 OR COX4A OR COX4.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/c; TISSUE=Heart;
RX MEDLINE=91057158; PubMed=2173832;
RA Grossman L.I., Akamatsu M.;
RT "Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c
oxidase.";
RT Nucleic Acids Res. 18:6454-6454(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91378465; PubMed=1654830;
RA Carter R.S., Avadhani N.G.;
RT "Cloning and characterization of the mouse cytochrome c oxidase
subunit IV gene.";
RL Arch. Biochem. Biophys. 288:97-106(1991).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.

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CC -1- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
CC -----
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CC -----
DR EMBL; M37831; AAB02139.1; -.
DR EMBL; M58034; AAB02139.1; JOINED.
DR EMBL; M37829; AAB02140.1; -.
DR EMBL; X54691; CAA38507.1; -.
DR PIR; S12142; S12142.
DR MGD; MG1:88473; Cox411.
DR GO; GO:0005739; C:mitochondrion; IDA.
DR InterPro; IPR004203; COX4.
DR Pfam; PF02936; COX4; 1.
KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 169 CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM
FT FT
FT CONFLICT 34 34 A -> R (IN REF. 1).
FT CONFLICT 71 71 S -> N (IN REF. 1).
FT CONFLICT 140 141 MQ -> IE (IN REF. 1; AAB02139 AND 2).
SQ SEQUENCE 169 AA; 19530 MW; D30B1DBBE14FDBEA CRC64;

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 68 ADWS 71

RESULT 22
CX41 RAT ID -CX41 RAT STANDARD; PRT; 169 AA.
AC P10888;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor
DE (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV).
GN COX4I1 OR COX4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA MEDLINE=89240039; PubMed=2541414;
RX Goto Y., Amuro N., Okazaki T.;
RT "Nucleotide sequence of cDNA for rat brain and liver cytochrome c
RT oxidase subunit IV";
RL Nucleic Acids Res. 17:2851-2851(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=89296488; PubMed=2544859;
RA Gopalan G., Droste M., Kadenbach B.;
RT "Nucleotide sequence of cDNA encoding subunit IV of cytochrome c
RT oxidase from fetal rat liver";
RL Nucleic Acids Res. 17:4376-4376(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90237079; PubMed=2159010;
RA Yamada M., Amuro N., Goto Y., Okazaki T.;
RT "Structural organization of the rat cytochrome c oxidase subunit IV
RT gene";

RL J. Biol. Chem. 265:7687-7692(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=90326528; PubMed=2165254;
RA Amuro N., Yamada M., Goto Y., Okazaki T.;
RT "Complete nucleotide sequence of the gene encoding rat cytochrome c
RT oxidase subunit IV";
RL Nucleic Acids Res. 18:3992-3992(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=91067442; PubMed=2174541;
RA Virbasius J.V., Scarpulla R.C.;
RT "The rat cytochrome c oxidase subunit IV gene family: tissue-specific
RT and hormonal differences in subunit IV and cytochrome c mRNA
RT expression";
RL Nucleic Acids Res. 18:6581-6586(1990).
RN [6]
RP SEQUENCE OF 23-32.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=9534529; PubMed=7601105;
RA Schaegger H., Noack H., Halanek W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform";
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC chains of cytochrome c oxidase, the terminal oxidase in
CC mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrion inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
CC -----
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CC -----
DR EMBL; X14209; CAA32426.1; -.
DR EMBL; X15029; CAA33133.1; -.
DR EMBL; J05425; AAA40949.1; -.
DR EMBL; X54081; CAA38018.1; -.
DR PIR; A35209; A35209.
DR InterPro; IPR004203; COX4.
DR Pfam; PF02936; COX4; 1.
KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
FT TRANSIT 1 22 MITOCHONDRION.
FT CHAIN 23 169 CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM
FT FT
SQ SEQUENCE 169 AA; 19514 MW; F0187C76B7A1A9FE CRC64;

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 68 ADWS 71

RESULT 23
RL18 HALN1 ID -RL18 HALN1 STANDARD; PRT; 182 AA.
AC P50562; Q9HPB5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L18P (Hsal18).
GN RPL18P OR VNG1714G. (strain NRC-1 / ATCC 700922 / JCM 11081), and
OS Halobacterium sp.

```
OS Halobacterium salinarum.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64094, 2242;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NRC-1;
RC MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Balliga N.S., Thorsson V., Shroona J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angvine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlachroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
RA "Genome sequence of Halobacterium species NRC-1.";
RT Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
[2]
RN SEQUENCE OF 1-23.
RP SPECIES=H. salinarum; STRAIN=DSM 3754;
RC MEDLINE=94229075; PubMed=8174557;
RA McDougall J., Wittmann-Liebold B.;
RT "Comparative analysis of the protein components from 5S rRNA.protein
complexes of halophilic archaeobacteria.";
RL Eur. J. Biochem. 221:779-785(1994).
CC -1- SIMILARITY: Belongs to the L18P family of ribosomal proteins.
-----
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-----
DR EMBL; AE005077; AAG19955.1; -.
DR PIR; G84323; G84323.
DR InterPro; IPR005484; Ribosomal_L18p.
DR Pfam; PF00863; Ribosomal_L18p.1.
KW Ribosomal protein; Complete proteome.
FT INIT_MET 0
SQ SEQUENCE 182 AA; 19680 MW; 1607FD9C5243288B CRC64;
Query Match 66.7%; Score 4; DB 1; Length 182;
Best Local Similarity 100.0%; Pred.No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
DB 137 ADWS 140
RESULT 24
ID YE21_AQUAE STANDARD; PRT; 197 AA.
AC 067415;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein AQ_1421.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=VF5;
RC MEDLINE=98196666; PubMed=9537320;
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
```

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RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- SIMILARITY: Belongs to the UPF0033 family.
-----
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-----
DR EMBL; AE000739; AAC07381.1; -.
DR PIR; E70423; E70423.
DR InterPro; IPR001455; UPF0033.
DR Pfam; PF01206; UPF0033; 1.
DR PROSITE; PS01148; UPF0033; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 197 AA; 22604 MW; 3E8E5E9147C11DF2 CRC64;
Query Match 66.7%; Score 4; DB 1; Length 197;
Best Local Similarity 100.0%; Pred.No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 WSWA 6
DB 51 WSWA 54
RESULT 25
ID HAM1_STRPN STANDARD; PRT; 200 AA.
AC Q97NX3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE HAM1 protein homolog.
GN SP1880 OR SPRI695.
OS Streptococcus pneumoniae, and
OC Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313, 171101;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC BAA-334 / TIGR4;
RC MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae.";
RN Science 293:498-506(2001).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=ATCC BAA-255 / R6;
RC MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rocky P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Steck P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5709-5717(2001).
```

CC CC -1- SIMILARITY: Belongs to the HAM1 NTPase family.

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CC -----

DR EMBL; AE007478; AAK75952.1; -.

DR EMBL; AE008534; AAL00498.1; ALT_INIT.

DR PIR; G95219; G95219.

DR TIGR; SP1880; -.

DR HAMAP; MF_01405; -; 1.

DR InterPro; IPR002637; Ham1p like.

DR Pfam; PF01725; Ham1p like; 1.

DR ProDom; PD004952; Ham1p like; 1.

DR TIGRFAMs; TIGR00042; TIGR00042; 1.

KW Hydrolyase; Complete proteome.

SQ SEQUENCE 200 AA; 22041 MW; 991DAC2C847D31A8 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

Db 135 ADWS 138

RESULT 26

TATB_XANAC

ID TATB_XANAC STANDARD; PRT; 208 AA.

AC Q8PEX3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sec-independent protein translocase protein tatB homolog.

GN TATB OR XAC4217.

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=2202145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardoso J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Perro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities".

RL Nature 417:459-463(2002).

CC -1- FUNCTION: Required for correct localization of precursor proteins

CC bearing signal peptides with the twin arginine conserved motif

CC S/T-R-X-F-L-K. This sec-independent pathway is termed TAT for

CC twin-arginine translocation system. This system mainly transports

CC proteins with bound cofactors that require folding prior to export

CC (By similarity).

CC -1- SUBCELLULAR LOCATION: Inner membrane-bound (Probable).

CC CC -1- SIMILARITY: Belongs to the tatB family.

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CC -----

DR EMBL; AE012074; AAM39052.1; -.

DR HAMAP; MF_00237; -; 1.

DR InterPro; IPR003369; MtaA_Hcf106.

DR InterPro; IPR003398; TatB.

DR Pfam; PF02416; MtaA_Hcf106; 1.

DR PRINTS; PR01506; TATBPROTEIN.

DR TIGRFAMs; TIGR01410; tatB; 1.

KW Transport; Protein transport; Translocation; Transmembrane;

KW Inner membrane; Complete proteome.

FT TRANSMEM 1 21 POTENTIAL.

SQ SEQUENCE 208 AA; 21971 MW; A9431BD2F2BE84F6 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 1.e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

Db 117 ADWS 120

RESULT 27

VNVCN_PAVBO

ID VNVCN_PAVBO STANDARD; PRT; 213 AA.

AC P07295;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last annotation update)

DE Probable noncapsid protein NP1.

OS Bovine parvovirus (BPV).

OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

OX NCBI_TaxID=10784;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=87061184; PubMed=3783814;

RA Chen K.C., Shull B.C., Moses E.A., Lederman M., Stout E.R.,

RA Bates R.C.;

RT "Complete nucleotide sequence and genome organization of bovine

RT parvovirus".

RL J. Virol. 60:1085-1097(1986).

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CC -----

DR EMBL; M14363; AAB59846.1; -.

DR PIR; B26104; UYVPPI.

KW Noncapsid protein.

SQ SEQUENCE 213 AA; 24834 MW; 768CB1E8F77C2626 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 213;

Best Local Similarity 100.0%; Pred. No. 1.e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4

Db 21 ADWS 24

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RESULT 28
RECO_PSESM          STANDARD;          PRT;   227 AA.
AC Q87XG3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE DNA repair protein reco (Recombination protein O).
GN RECO OR PSPT04215.
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,
RA Van Aken S.E., Feldblyum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,
RA Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,
RA Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,
RA White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Involved in DNA repair and recF pathway recombination
CC (By similarity).
CC -1- SIMILARITY: Belongs to the reco family.
CC -----
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CC -----
DR EMBL; AE016871; AA057671.1; -.
DR TIGR; PSPT04215; -.
DR HAMAP; MF_00201; -.
DR InterPro; IPR003717; RecO.
DR Pfam; PF02565; RecO; 1.
KW DNA repair; DNA recombination; Complete proteome.
SQ SEQUENCE 227 AA; 24930 MW; 43A1D9D6AE6BF6FC CRC64;
-----
Query Match 66.7%; Score 4; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
DB 190 ADWS 193
|||||
RESULT 29
RECO_PSEAE          STANDARD;          PRT;   233 AA.
AC Q9XCX7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA repair protein reco (Recombination protein O).
GN RECO OR PA0772.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=PAK;
RX MEDLINE=99369891; PubMed=10438789;
RA Powell B.S., Peters H.K. III, Nakamura Y., Court D.L.;
RT "Cloning and analysis of the rnc-era-reco operon from Pseudomonas
RT aeruginosa."
RL J. Bacteriol. 181:5111-5113(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Involved in DNA repair and recF pathway recombination
CC (By similarity).
CC -1- SIMILARITY: Belongs to the reco family.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 196.
CC -----
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CC -----
DR EMBL; AF123492; AAD40231.1; ALT_FRAME.
DR EMBL; AE004512; AAG04161.1; -.
DR PIR; G83548; G83548.
DR HAMAP; MF_00201; -.
DR InterPro; IPR003717; RecO.
DR Pfam; PF02565; RecO; 1.
KW DNA repair; DNA recombination; Complete proteome.
SQ SEQUENCE 233 AA; 25498 MW; 67ABBE6BCD82DC1A CRC64;
-----
Query Match 66.7%; Score 4; DB 1; Length 233;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWS 4
DB 190 ADWS 193
|||||
RESULT 30
UBIE_LISMO          STANDARD;          PRT;   237 AA.
AC Q92A77;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Menquinone biosynthesis methyltransferase ubiE (EC 2.1.1.-).
GN UBIE OR LMO1931 OR LIN2045
OS Listeria monocytogenes, and
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639, 1642;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=L.monocytogenes, and L.innocua;
RC STRAIN=EGD-e / Serovar 1/2a, and CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
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RA Entian K.-D., Psihi H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunat F., Kurapkat G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordsiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schluter T., Smoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,
 RT "Comparative genomics of *Listeria* species.";
 RL Science 294:849-852(2001).
 CC -1- FUNCTION: Methyltransferase required for the conversion of
 CC dimethylmenaquinone (DMKH2) to menaquinone (MKH2) (By similarity).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + demethylmenaquinol =
 CC S-adenosyl-L-homocysteine + menaquinol.
 CC -1- PATHWAY: Menaquinone biosynthesis; last step.
 CC -1- SIMILARITY: Belongs to the ubiE family.
 CC -----
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 CC -----
 DR EMBL; AL591981; CAD00009.1; -;
 DR EMBL; AL596170; CAC97275.1; -;
 DR PIR; AC1316; AC1316.
 DR PIR; AC1688; AC1688.
 DR Listidat; LIN02045; -;
 DR Listidat; LMO01931; -;
 DR HAMAP; MF_01813; -; 1.
 DR InterPro; IPR001601; Methyltransf.
 DR InterPro; IPR000051; SAM bind.
 DR InterPro; IPR004034; Ubi7/men Mettransf.
 DR InterPro; IPR004033; UbiE/COQ5 Metrf.
 DR Pfam; PF01209; Ubie_methyltran; 1.
 DR PROSITE; PS01183; UBI_E_1; 1.
 DR PROSITE; PS01184; UBI_E_2; FALSE NEG.
 DR Menaquinone biosynthesis; Transferrase; Methyltransferase;
 KW Complete proteome.
 SQ SEQUENCE 237 AA; 27330 MW; 3363669F83D9AC74 CRC64;

 Query Match 66.7%; Score 4; DB 1; Length 237;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWS 4
 DB 59 ADWS 62

 RESULT 31
 TAM_RHILO
 ID TAM_RHILO STANDARD; PRT; 256 AA.
 AC Q98K73; 2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Trans-aconitate 2-methyltransferase (EC 2.1.1.144).
 GN TAM OR MLL1606.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303059;
 RX MEDLINE=21082930; PubMed=11214969;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idehara K., Ishikawa A., Kawahara K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 CC -1- FUNCTION: Catalyzes the S-adenosylmethionine monomethyl
 CC esterification of trans-aconitate (By similarity).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + trans-aconitate = S-
 CC adenosyl-L-homocysteine + (E)-3-(methoxycarbonyl)pent-2-enedioate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the methyltransferase superfamily. Tam
 CC family.
 CC -----
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 CC -----
 DR EMBL; AP002397; BAB48941.1; -;
 DR HAMAP; MF_00560; -; 1.
 DR InterPro; IPR000051; SAM bind.
 DR Transferrase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 256 AA; 28539 MW; AA87B101141B4608 CRC64;

 Query Match 66.7%; Score 4; DB 1; Length 256;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWS 4
 DB 2 ADWS 5

 RESULT 32
 YK09_RALSO
 ID YK09_RALSO STANDARD; PRT; 257 AA.
 AC Q8XV4; 2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hypothetical UPF0246 protein RSC2009.
 GN RSC2009 OR RS03577.
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GM11000;
 RX MEDLINE=21681879; PubMed=11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
 RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
 RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
 RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
 RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
 RA Weissbach J., Boucher C.A.;
 RT "Genome sequence of the plant pathogen *Ralstonia solanacearum*.";
 RL Nature 415:497-502(2002).
 CC -1- SIMILARITY: Belongs to the UPF0246 family.
 CC -----
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 CC -----
 DR EMBL; AL646067; CAD15711.1; -;
 DR HAMAP; MF_00652; -; 1.
 DR InterPro; IPR005583; DUF328.
 DR Pfam; PF03883; DUF328; 1.

```
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 257 AA; 28974 MW; 8E44372F7FDD7F3A CRC64;

Query Match 66.7%; Score 4; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
   ||||
DB 65 ADWS 68

RESULT 33
ID DET2 ARATH STANDARD; PRT; 262 AA.
AC Q3944; Q3SH83;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable steroid reductase DET2 (EC 1.3.99.-).
GN DET2 OR AT2G38050 OR T8P21.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=96185496; PubMed=8602526;
RA Li J., Nagpal P., Vitart V., Morris T.C., Chory J.;
RT "A role for brassinosteroids in light-dependent development of
  Arabidopsis.";
RL Science 272:398-401(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Rensing C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
  thaliana.";
RL Nature 402:761-768(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Hayao Q., Choy N., Enju N., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tanse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
  genome.";
RL Science 302:842-846(2003).
CC -1- FUNCTION: Probably involved in a reduction step in the
  biosynthesis of the plant steroid, brassinolide. Defects in DET2
  leads to defects in light-regulated development.
CC -1- PATHWAY: Brassinolide biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
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CC -1- SIMILARITY: Belongs to the steroid 5-alpha reductase family.
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-----
DR EMBL; U53860; AAC49264.1; -.
DR EMBL; AC007661; AAD32767.1; -.
DR EMBL; AY045926; AAK76600.1; -.
DR EMBL; AY079337; AAL85068.1; -.
DR PIR; C84800; C84800.
DR InterPro; IPR001104; Strd5A_dhc.
DR Pfam; PF02544; Steroid_dh; 1.
DR PROSITE; PS0244; S5A_REDUCTASE; 1.
KW Oxidoreductase; Transmembrane.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 51 71 POTENTIAL.
FT TRANSMEM 113 133 POTENTIAL.
FT TRANSMEM 148 168 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT CONFLICT 198 198 C -> R (IN REF. 1).
SQ SEQUENCE 262 AA; 30635 MW; 88291B8A8AF5664 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 262;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
   ||||
DB 216 WSWA 219

RESULT 34
CY1_RHURU STANDARD; PRT; 272 AA.
AC P23135;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c1 precursor.
GN P2C.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1085;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 25-50.
RC STRAIN=PR1;
RX MEDLINE=91094774; PubMed=2176269;
RA Majewski C., Trebst A.;
RT "The pet genes of the Rhodospirillum rubrum: cloning and sequencing of
  the genes for the cytochrome bcl-complex.";
RL Mol. Gen. Genet. 224:373-382(1990).
CC -1- FUNCTION: Component of the ubiquinol-cytochrome c reductase
  complex (complex III or cytochrome b-c1 complex), which is a
  respiratory chain that generates an electrochemical potential
  coupled to ATP synthesis.
CC -1- SUBUNIT: The main subunits of complex b-c1 are: cytochrome b,
  cytochrome c1 and the Rieske protein.
-----
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DR EMBL; X55387; CAA39060.1; -.

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DR PIR; S12258; CCOF1R.
DR InterPro; IPR002326; Cyt Cl.
DR Pfam; PF02167; Cytochrome C1; 1.
DR PRINTS; PR00603; CYTOCHROME_C1.
DR PROSITE; PS00190; CYTOCHROME_C_1.
KW Electron transport; Respiratory chain; Heme; Transmembrane; Signal.
FT SIGNAL 1 24
FT CHAIN 25 272 CYTOCHROME C1.
FT BINDING 61 61 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 64 64 HEME (COVALENT) (BY SIMILARITY).
FT METAL 65 65 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 200 200 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 244 261 ANCHORS TO THE MEMBRANE (POTENTIAL).
SQ SEQUENCE 272 AA; 29494 MW; D2575CEB57CC9332 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 35 DWSW 38

RESULT 35
HRP5 HUMAN
ID -HRP5_HUMAN STANDARD; PRT; 279 AA.
AC Q96KN8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE H-rev107-like protein 5.
GN HRLP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RA Hughes P.J., Stanway G.;
RT "Identification of a novel member of the H-rev107 protein family.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the H-rev107 family.
CC
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CC
CC -----
CC EMBL; AJ416558; CAC94942.1; -.
CC InterPro; IPR007053; NC.
CC Pfam; PF04970; NC; 1.
CC SEQUENCE 279 AA; 30281 MW; F6CC44996B0A8E3D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 105 ADWS 108

RESULT 36
CHR2_PSEAE
ID -CHR2_PSEAE STANDARD; PRT; 280 AA.
AC Q916V7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chemotaxis protein methyltransferase 2 (EC 2.1.1.80).
GN CHER2 OR PA0175.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN 1
RP SEQUENCE FROM N.A.
RA STRAIN=ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964 (2000).
CC -1- FUNCTION: METHYLATION OF THE MEMBRANE-BOUND METHYL-ACCEPTING
CC CHEMOTAXIS PROTEINS (MCP) TO FORM GAMMA-GLUTAMYL METHYL ESTER
CC RESIDUES IN MCP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + protein L-glutamate
CC = S-adenosyl-L-homocysteine + protein L-glutamate methyl ester.
CC -1- SIMILARITY: Contains 1 cher-type methyltransferase domain.
CC
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CC
CC -----
CC EMBL; AE004455; AAG03565.1; -.
CC PIR; H83623; H83623.
CC HSP; P07801; IAF7.
CC InterPro; IPR000780; Cher Metranf.
CC InterPro; IPR001601; Methyltransf.
CC Pfam; PF01739; Cher; 1.
CC Pfam; PF03705; Cher N. 1.
CC PRINTS; PR00996; CHERMTFRASE.
CC SMART; SM00138; Metrc; 1.
CC PROSITE; PS0123; CHER; 1.
KW Transferase; Methyltransferase; Complete proteome.
FT DOMAIN 10 280 CHER-TYPE METHYLTRANSFERASE.
SQ SEQUENCE 280 AA; 32028 MW; FD2AF1491DDC57FB CRC64;

Query Match 66.7%; Score 4; DB 1; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 212 ADWS 215

RESULT 37
3MG2_ECOLI
ID -3MG2_ECOLI STANDARD; PRT; 282 AA.
AC P04395;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-3-methyladenine glycosylase II (EC 3.2.2.21) (3-methyladenine-DNA
DE glycosylase II, inducible) (TAG II) (DNA-3-methyladenine glycosidase
DE II).
GN ALKA OR AIDA OR B2068.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
```



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FT TURN 275 276
SQ SEQUENCE 282 AA; 31393 MW; B66BB5E23010989C CRC64;

Query Match 66.7%; Score 4; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 11 DWSW 14

RESULT 38
RP32_PSEAE STANDARD; PRT; 284 AA.
AC P42378;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE RNA polymerase sigma-32 factor.
GN RPOH OR PA0376.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=95245923; PubMed=7728657;
RA Naczynski Z.M., Mueller C., Kropinski A.M.;
RT "Cloning the gene for the heat shock response positive regulator
RL (sigma 32 homolog) from Pseudomonas aeruginosa.";
RN Can. J. Microbiol. 41:75-87(1995).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=95212932; PubMed=7698670;
RA Benveniste L., Koby S., Rutman A., Giladi H., Yura T.,
RA Oppenheim A.B.;
RT "Cloning and primary sequence of the rpoH gene from Pseudomonas
RL aeruginosa.";
RN Gene 155:73-76(1995).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz R.L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED. THIS SIGMA FACTOR IS RESPONSIBLE FOR THE
CC EXPRESSION OF HEAT SHOCK PROMOTERS (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the sigma-70 factor family. Sigma-32
CC subfamily.
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CC -----
CC EMBL; U09560; AAA92723.1; -
CC EMBL; S77322; AAB33935.1; -
CC EMBL; D50052; BAA08769.1; -
CC EMBL; AE004475; AAG03765.1; -
CC PIR; JC4040; JC4040.
CC HSP; P00579; ISIG.
CC InterPro; IPR009043; RNA_pol_sigma.
CC InterPro; IPR007627; Sigma70_r2.
CC InterPro; IPR007630; Sigma70_r4.
CC InterPro; IPR009043; Sigma70.
CC Pfam; PF04542; sigma70_r2; 1.
CC Pfam; PF04545; sigma70_r4; 1.
CC PRINTS; PR00046; SIGMA70F0CT.
CC PROSITE; PS00715; SIGMA70_1; 1.
CC PROSITE; PS00716; SIGMA70_2; 1.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Heat shock; Complete proteome.
FT DOMAIN 77 90 POLYMERASE CORE BINDING (POTENTIAL).
FT DNA_BIND 253 272 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 284 284 A -> G (IN REF. 1).
SQ SEQUENCE 284 AA; 32581 MW; 282395BE38F21D5D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 216 ADWS 219

RESULT 39
P01_RHOBL STANDARD; PRT; 289 AA.
AC P39767;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Porin.
GN OPMA.
OS Rhodopseudomonas blastica.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1075;
RN [1]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=94191532; PubMed=8142898;
RA Kreusch A., Neubueser A., Schiltz E., Weckesser J., Schulz G.E.;
RT "Structure of the membrane channel porin from Rhodopseudomonas
RL blastica at 2.0-A resolution.";
RN Protein Sci. 3:58-63(1994).
[2]
RX X-RAY CRYSTALLOGRAPHY (1.96 ANGSTROMS).
RP MEDLINE=95055730; PubMed=7525973;
RA Kreusch A., Schulz G.E.;
RT "Refined structure of the porin from Rhodopseudomonas blastica.
RT Comparison with the porin from Rhodobacter capsulatus.";
RL J. Mol. Biol. 243:891-905(1994).
[3]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF MUTANTS.
RP MEDLINE=98348035; PubMed=9684893;
RA Schmid B., Maveyraud L., Kromer M., Schulz G.E.;
RT "Porin mutants with new channel properties.";
RL Protein Sci. 7:1603-1611(1998).
CC -1- FUNCTION: FORMS CHANNELS THAT ALLOW THE PASSIVE DIFFUSION OF SMALL
CC HYDROPHILIC SOLUTIONS UP TO AN EXCLUSION LIMIT OF ABOUT 0.6 kDa.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.
CC PIR; S38806; S38806.
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DR PDB; 1PRN; 24-OCT-94.
DR PDB; 2PRN; 13-JAN-99.
DR PDB; 3PRN; 12-AUG-98.
DR PDB; 4PRN; 12-AUG-98.
DR PDB; 5PRN; 12-AUG-98.
DR PDB; 6PRN; 12-AUG-98.
DR PDB; 7PRN; 12-AUG-98.
DR PDB; 8PRN; 12-AUG-98.
DR PDB; 1BH3; 12-AUG-98.
DR PDB; 1H6S; 12-DEC-02.
DR InterPro; IPR001702; Porin Gram-ve.
DR Pfam; PF00267; Gram-ve_porins; 1.
KW Outer membrane; Transmembrane; Porin; 3D-structure.
FT STRAND 2 15
FT TURN 16 17
FT TURN 20 21
FT STRAND 25 39
FT TURN 42 43
FT STRAND 46 56
FT TURN 57 58
FT TURN 60 62
FT STRAND 66 66
FT STRAND 70 75
FT TURN 76 77
FT STRAND 78 83
FT HELIX 88 91
FT TURN 95 98
FT STRAND 100 100
FT TURN 101 104
FT STRAND 105 105
FT TURN 107 108
FT TURN 123 124
FT TURN 126 129
FT STRAND 131 138
FT STRAND 142 150
FT TURN 151 154
FT HELIX 157 159
FT STRAND 163 171
FT STRAND 175 183
FT HELIX 185 187
FT TURN 189 190
FT STRAND 193 200
FT STRAND 206 214
FT TURN 216 217
FT TURN 219 220
FT STRAND 223 232
FT TURN 233 234
FT STRAND 235 244
FT TURN 247 248
FT STRAND 252 262
FT TURN 263 264
FT STRAND 265 273
FT TURN 275 276
FT STRAND 279 289
SQ SEQUENCE 289 AA; 30597 MW; 08252D9803A1044C CRC64;

Query Match 66.7%; Score 4; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 168 ADWS 171

RESULT 40
C552_PSEST STANDARD; PRT; 291 AA.
AC P24037;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome c-552 precursor.
GN NIRB.

OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=91160715; PubMed=2001732;
RA Juengst A., Wakabayashi S., Matsubara H., Zumft W.G.;
RT "the nirSTBM region coding for cytochrome cdi-dependent nitrite
RT respiration of Pseudomonas stutzeri consists of a cluster of mono-,
RL di-, and tetraheme proteins.";
RL FEBS Lett. 279:205-209(1991).
RN [2]
RP SEQUENCE OF 24-270.
RC STRAIN=ATCC 14405 / Zobell;
RX MEDLINE=89192360; PubMed=2539041;
RA Denariatz C.M., Liu M.-Y., Payne W.J., le Gall J., Marquez L.,
RA Dunford H.B., van Beeumen J.;
RT "Cytochrome c peroxidase activity of a protease-modified form of
RT cytochrome c-552 from the denitrifying bacterium Pseudomonas
RT perfectomarina.";
RL Arch. Biochem. Biophys. 270:114-125(1989).
CC -1- FUNCTION: May play a role in nitrite reduction. Shows peroxidase
CC activity on proteolytic modification.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- INDUCTION: By anaerobic conditions.
CC -1- PTM: Binds 2 heme groups per molecule.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X56813; CAA40152.1; -.
DR PIR; S13938; CQPS2S.
DR InterPro; IPR000345; CytC heme BS.
DR PROSITE; PS00190; CYTOCHROME C_1.
KW Electron transport; Heme; Repeat; Periplasmic; Signal.
FT SIGNAL 1 23
FT CHAIN 24 291 CYTOCHROME C-552.
FT BINDING 68 68 HEME 1 (COVALENT) (BY SIMILARITY).
FT BINDING 71 71 HEME 1 (COVALENT) (BY SIMILARITY).
FT METAL 72 72 IRON (HEME 1 AXIAL LIGAND)
FT (BY SIMILARITY).
FT BINDING 157 157 HEME 2 (COVALENT) (BY SIMILARITY).
FT BINDING 161 161 HEME 2 (COVALENT) (BY SIMILARITY).
FT METAL 162 162 IRON (HEME 2 AXIAL LIGAND)
FT (BY SIMILARITY).
FT CONFLICT 59 59 A -> D (IN REF. 2).
FT CONFLICT 229 229 D -> N (IN REF. 2).
FT CONFLICT 268 270 RYH -> SYN (IN REF. 2).
SQ SEQUENCE 291 AA; 30426 MW; DB34BC903CD2687F CRC64;

Query Match 66.7%; Score 4; DB 1; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 27 ADWS 30

RESULT 41
RSP4_BOVIN STANDARD; PRT; 295 AA.
ID RSP4_BOVIN
AC P26452;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
```

40S ribosomal protein P40 (C10 protein).
LAWR1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nuchal ligament;
RA MEDLINE=91182754; PubMed=1849001;
RX Grosso L.E., Park P.W., Mecham R.P.;
RT "Characterization of a putative clone for the 67-kilodalton
RT elastin/laminin receptor suggests that it encodes a cytoplasmic
RL Biochemistry 30:3346-3350(1991).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -1- CAUTION: Was originally thought to be a laminin receptor.
CC
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CC
CC EMBL; M64923; AAA62713.1; -.
DR PIR; A38464; A38464.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PRINTS; PR00395; RIBOSOMALS2.
DR TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Repeat.
FT REPEAT 247 249 MOTIF A (DWS).
FT REPEAT 266 268 MOTIF A (DWS).
FT REPEAT 275 277 MOTIF A (DWS).
FT REPEAT 264 269 MOTIF B (TEDWSA).
FT REPEAT 273 278 MOTIF B (TEDWSA).
FT REPEAT 285 287 MOTIF C (TEW).
FT REPEAT 292 294 MOTIF C (TEW).
SQ SEQUENCE 295 AA; 32897 MW; 4CAD2FB358BF82C5 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 246 ADWS 249

RESULT 42
RSP4_CRIGR STANDARD; PRT; 295 AA.
AC P39982,1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).
GN LAWR1.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;

Chen M.S.M., Laszlo A.A.;
Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC -1- CAUTION: Was originally thought to be a laminin receptor.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L16589; AAB46394.1; -.
DR EMBL; Z22749; CAA80434.1; -.
DR PIR; S33438; S33438.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR005707; Ribosomal_S2_e/a.
DR Pfam; PF00318; Ribosomal_S2; 1.
DR PRINTS; PR00395; RIBOSOMALS2.
DR TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW Ribosomal protein; Repeat.
FT REPEAT 247 249 MOTIF A (DWS).
FT REPEAT 266 268 MOTIF A (DWS).
FT REPEAT 275 277 MOTIF A (DWS).
FT REPEAT 264 269 MOTIF B (TEDWSA).
FT REPEAT 273 278 MOTIF B (TEDWSA).
FT REPEAT 285 287 MOTIF C (TEW).
FT REPEAT 292 294 MOTIF C (TEW).
SQ SEQUENCE 295 AA; 32881 MW; 3E43B4CB01828643 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 246 ADWS 249

RESULT 43
RSP4_HUMAN STANDARD; PRT; 295 AA.
ID RSP4_HUMAN
AC P08855; P11085; P12030; Q16471;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor) (Colon
DE carcinoma laminin-binding protein) (NEW/1CHD4) (Multidrug resistance-
DE associated protein MGR1-Ag).
GN LAWR1 OR LAMBR OR RPSA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88320449; PubMed=2970639;
RA Yow H., Wong J.M., Chen H.S., Lee C., Steele G.D. Jr., Chen L.B.;
RT "Increased mRNA expression of a laminin-binding protein in human
RT colon carcinomas: complete sequence of a full-length cDNA encoding the
RT protein".
RL Proc. Natl. Acad. Sci. U.S.A. 85:6394-6398(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89282388; PubMed=2543954;
RA van den Ouweland A.M.W., van Duijnhoven H.L.P., Deichmann K.A.,
RA van Groningen J.J.M., de Leij L., van de Ven W.J.M.;
RT "Characteristics of a multicopy gene family predominantly consisting
RT of processed pseudogenes.";

RL	Nucleic Acids Res. 17:3829-3843 (1989).	RN	SEQUENCE OF 225-295 FROM N.A.
RP	SEQUENCE FROM N.A.	RP	MEDLINE=98248690; PubMed=9582194;
RX	MEDLINE=96330329; PubMed=8760291;	RX	Kenmochi N., Kawaguchi T., Rozen S., Davis E., Goodman N.,
RA	Jackers P., Minolletti F., Belotti D., Clausse N., Sozzi G.,	RA	Hudson T.J., Tanaka T., Page D.C.;
RA	Sobel M.E., Casironovo V.;	RA	"A map of 75 human ribosomal protein genes.";
RA	"Isolation from a multigene family of the active human gene of the	RL	Genome Res. 8:509-523 (1998).
RT	metastasis-associated multifunctional protein 37LRP/p40 at chromosome	CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.
RT	3p21.3.";	CC	-1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
RL	Oncogene 13:495-503 (1996).	CC	-1- CAUTION: Was originally thought to be a laminin receptor.
[4]		CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
RP	SEQUENCE FROM N.A.	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP	TISSUE=Lung;	CC	the European Bioinformatics Institute. There are no restrictions on its
RX	MEDLINE=92282574; PubMed=1534510;	CC	use by non-profit institutions as long as its content is in no way
RA	Sachon K., Narumi K., Sakai T., Abe T., Kikuchi T., Matsushima K.,	CC	modified and this statement is not removed. Usage by and for commercial
RA	Sindoh S., Motomiya M.;	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
RT	"Cloning of 67-kDa laminin receptor cDNA and gene expression in	CC	or send an email to license@isb-sib.ch).
RT	normal and malignant cell lines of the human lung.";	CC	
RL	Cancer Lett. 62:199-203 (1992).	CC	
[5]		DR	EMBL; J03799; AAA36161.1; -
RP	SEQUENCE FROM N.A.	DR	EMBL; X15005; CAA33112.1; -
RA	Shi Y., Zhai H., Wang X., Wu H., Ning X., Han Y., Zhang D., Xiao B.,	DR	EMBL; U43901; AAC30652.1; -
RA	Wu K., Fan D.;	DR	EMBL; S37431; AAB22299.1; -
RT	"Multidrug resistance associated protein Mgr1-Ag is identical to human	DR	EMBL; AF503367; AAM33304.1; -
RT	67-kDa laminin receptor precursor.";	DR	EMBL; BC005391; AAH05391.1; -
RL	Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.	DR	EMBL; BC008867; AAH08867.1; -
[6]		DR	EMBL; BC009974; AAH09974.1; -
RP	SEQUENCE FROM N.A.	DR	EMBL; BC010054; AAH10054.1; -
RP	TISSUE=Brain, Cervix, Muscle, Placenta, Urinary bladder, and Uterus;	DR	EMBL; BC010418; AAH10418.1; -
RX	MEDLINE=22388257; PubMed=12477932;	DR	EMBL; BC013827; AAH13827.1; -
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,	DR	EMBL; BC015654; AAH15654.1; -
RA	Strausberg R.L., Feingold F.S., Wagner L., Shenmen C.M., Schuler G.D.,	DR	EMBL; BC034537; AAH34537.1; -
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	DR	EMBL; BC053370; AAH53370.1; -
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	DR	EMBL; M14199; AAA36165.1; -
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	DR	EMBL; X61156; CAA43469.1; -
RA	Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,	DR	EMBL; U36484; AAC50313.1; -
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	DR	EMBL; AB007146; BAA25812.1; -
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	DR	PIR; A31233; A31233.
RA	Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	DR	Genew; HGNC:6502; LAMR1.
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	DR	MM; 150370; -
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	DR	GO; GO:0005055; Filaminin receptor activity; TAS.
RA	Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,	DR	InterPro; IPR001865; Ribosomal_S2_e/a.
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	DR	InterPro; IPR005707; Ribosomal_S2; 1.
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	DR	PRINTS; PR00395; RIBOSOMAL_S2.
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	DR	TIGRFAMS; TIGR01012; Sa S2 E A; 1.
RA	Butterfield Y.S.N., Krzyzowski M.I., Skalska U., Smalhus D.E.,	DR	PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	DR	PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
RT	"Generation and initial analysis of more than 15,000 full-length	KW	Ribosomal protein; Repeat.
RT	human and mouse cDNA sequences.";	FT	REPEAT 247 249 MOTIF A (DWS).
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	FT	REPEAT 266 268 MOTIF A (DWS).
[7]		FT	REPEAT 275 277 MOTIF A (DWS).
RP	SEQUENCE OF 161-295 FROM N.A.	FT	REPEAT 264 269 MOTIF B (TEDWSA).
RX	MEDLINE=87016902; PubMed=2429301;	FT	REPEAT 273 278 MOTIF B (TEDWSA).
RA	Wewer U.M., Liotta L.A., Jaye M., Ricca G.A., Drohan W.N.,	FT	REPEAT 285 287 MOTIF C (TEW).
RA	Clayson A.P., Rao C.N., Wirth P., Colligan J.E., Albrechtsen R.,	FT	REPEAT 292 294 L -> V (IN REF. 8).
RA	Mudryj M., Sobel M.E.;	FT	CONFLICT 60 60 Q -> QVCGTV (IN REF. 2).
RT	"Altered levels of laminin receptor mRNA in various human carcinoma	FT	CONFLICT 84 84 E -> G (IN REF. 4).
RT	cells that have different abilities to bind laminin.";	FT	CONFLICT 211 211 Q -> L (IN REF. 4).
RL	Proc. Natl. Acad. Sci. U.S.A. 83:7137-7141 (1986).	FT	CONFLICT 228 228 Q -> L (IN REF. 4).
[8]		SQ	SEQUENCE 295 AA; 32854 MW; C68DDDB16B759E79E CRC64;
RP	SEQUENCE OF 11-295 FROM N.A.		Query Match 66.7%; Score 4; DB 1; Length 295;
RA	Siyanova E.Y., Lukashev V.A., Blinov V.M., Troyanovskii S.M.;		Best Local Similarity 100.0%; Pred. No. 1.4e+02;
RT	"Determination and analysis of the primary sequence of human		Matches 4; Conservative 0; Mismatches 0; Indels 0;
RT	laminin-binding protein.";		
RL	Doki. Biochem. 313:227-231 (1990).		
[9]		Qy	1 ADWS 4
RP	SEQUENCE OF 85-209 FROM N.A.		Db
RP	TISSUE=Blood;		246 ADWS 249
RX	MEDLINE=96163906; PubMed=8596453;		
RA	Selvamurugan N., Ellicei G.L.;		
RT	"The gene for human E2 small nucleolar RNA resides in an intron of a		
RT	laminin-binding protein gene.";		
RL	Genomics 30:400-401 (1993).		


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RESULT 45
RSP4_MOUSE
ID RSP4_MOUSE STANDARD; PRT; 295 AA.
AC P14206;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).
GN LAMR1 OR P40-8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90057447; PubMed=2531008;
RA Rao C.N., Castronovo V., Schmitt M.C., Wewer U.M., Clayesmith A.P.,
RA Liotta L.A., Sobel M.E.;
RT "Evidence for a precursor of the high-affinity metastasis-associated
RT murine laminin receptor."
RL Biochemistry 28:7476-7486(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88189839; PubMed=3357791;
RA Makrides S., Chitpatima S.T., Bandyopadhyay R., Brawerman G.;
RT "Nucleotide sequence for a major messenger RNA for a 40 kilodalton
RT polypeptide that is under translational control in mouse tumor
RT cells."
RL Nucleic Acids Res. 16:2349-2349(1988).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the S2p family of ribosomal proteins.
CC -1- CAUTION: Was originally thought to be a laminin receptor.
CC
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CC
CC -----
CC EMBL; J02870; AAA39413.1; -.
CC EMBL; X06406; CAA29696.1; -.
CC SWISS-2DPAGE; P14206; MOUSE.
CC PMMA-2DPAGE; P14206; -.
CC MGD; MGI:105381; Lamr1.
CC InterPro; IPR001865; Ribosomal_S2.
CC InterPro; IPR005707; Ribosomal_S2_e/a.
CC PRINTS; PR00395; RIBOSOMALS2.
CC TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
CC PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
CC PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
CC Ribosomal protein; Repeat.
CC REPEAT 247 249 MOTIF A (DWS).
CC REPEAT 266 268 MOTIF A (DWS).
CC REPEAT 275 277 MOTIF A (DWS).
CC REPEAT 264 269 MOTIF B (TEDWSA).
CC REPEAT 273 278 MOTIF B (TEDWSA).
CC REPEAT 285 287 MOTIF C (TEW).
CC REPEAT 292 294 MOTIF C (TEW).
CC CONFLICT 18 18 L -> F (IN REF. 2).
CC CONFLICT 155 155 A -> R (IN REF. 2).
CC SEQUENCE 295 AA; 32719 MW; 449C7E36CF1F1931 CRC64;
Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWS 4
Db 246 ADWS 249
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RESULT 45
RSP4_RAT
ID RSP4_RAT STANDARD; PRT; 295 AA.
AC P38983;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 40S ribosomal protein SA (P40) (34/67 kDa laminin receptor).
GN LAMR1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=94164296; PubMed=8119397;
RA Tohgo A., Takasawa S., Munakata H., Yonekura H., Hayashi N.,
RA Okamoto H.;
RT "Structural determination and characterization of a 40 kDa protein
RT isolated from rat 40 S ribosomal subunit."
RL FEBS Lett. 340:133-138(1994).
RN [2]
RP SEQUENCE OF 199-295 FROM N.A.
RX STRAIN=Holtzman; TISSUE=Intestinal epithelium;
RX MEDLINE=94357375; PubMed=8076763;
RA Rao M., Manishen W.J., Maheshwari Y., Sykes D.E., Siyanova E.Y.,
RA Tyner A.L., Weiser M.M.;
RT "Laminin receptor expression in rat intestine and liver during
RT development and differentiation."
RL Gastroenterology 107:764-772(1994).
RN [3]
RP SEQUENCE OF 226-295 FROM N.A.
RA Burns F.R., Rajnavolgy E., Yamashita K., Li X., Shen N.,
RA Heber-Katz E.;
RL Submitted (SEP-1989) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the S2p family of ribosomal proteins.
CC -1- CAUTION: Was originally thought to be a laminin receptor.
CC
CC -----
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CC
CC -----
CC EMBL; D25224; BAA04953.1; -.
CC EMBL; U04942; AAB60453.1; -.
CC EMBL; M27798; AAA41509.1; -.
CC PIR; S42405; S42405.
CC InterPro; IPR001865; Ribosomal_S2.
CC InterPro; IPR005707; Ribosomal_S2_e/a.
CC Pfam; PF00318; Ribosomal_S2; 1.
CC PRINTS; PR00395; RIBOSOMALS2.
CC TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
CC PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
CC PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
CC Ribosomal protein; Repeat.
CC REPEAT 247 249 MOTIF A (DWS).
CC REPEAT 266 268 MOTIF A (DWS).
CC REPEAT 275 277 MOTIF A (DWS).
CC REPEAT 264 269 MOTIF B (TEDWSA).
CC REPEAT 273 278 MOTIF B (TEDWSA).
CC REPEAT 285 287 MOTIF C (TEW).
CC REPEAT 292 294 MOTIF C (TEW).
CC SEQUENCE 295 AA; 32824 MW; D7DD887DBDD340C CRC64;
Query Match 66.7%; Score 4; DB 1; Length 295;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 ADWS 4
Db      246 ADWS 249

RESULT 46
RSP4_CHK
ID_RSP4_CHK  STANDARD;      PRT;      296 AA.
AC  P50890;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  40S ribosomal protein SA (P40) (34/67 kDa laminin receptor) (37LRP).
OS  Gallus gallus (Chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC  Gallus.
OX  NCBI_TaxID=9031;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=white leghorn; TISSUE=Spleen;
RX  MEDLINE=97138089; PubMed=8985115;
RA  Clause N., Jackers P., Jares P., Joris B., Sobel M.E., Castronovo V.;
RT  "Identification of the active gene coding for the
RL  metastasis-associated 37LRP/p40 multifunctional protein.";
RL  DNA Cell Biol. 15:1009-1023(1996).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -1- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL: X94368; CAA64147.1; -.
DR  InterPro; IPR001865; Ribosomal_S2.
DR  InterPro; IPR005707; Ribosomal_S2_e/a.
DR  Pfam; PF00318; Ribosomal_S2; 1.
DR  PRINTS; PR00395; RIBOSOMALS2.
DR  TIGRFAMs; TIGR01012; Sa_S2_E_A; 1.
DR  PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
DR  PROSITE; PS00963; RIBOSOMAL_S2_2; 1.
KW  Ribosomal protein; Repeat.
FT  REPEAT 248 250      MOTIF A (DWS).
FT  REPEAT 248 250      MOTIF A (DWS).
FT  REPEAT 267 269      MOTIF A (DWS).
FT  REPEAT 276 278      MOTIF A (DWS).
FT  REPEAT 265 270      MOTIF B (TEDWSA).
FT  REPEAT 274 279      MOTIF B (TEDWSA).
FT  REPEAT 286 288      MOTIF C (TEW).
FT  REPEAT 293 295      MOTIF C (TEW).
SQ  SEQUENCE 296 AA; 33021 MW; 3486A86EF514E5CD CRC64;

Query Match      66.7%; Score 4; DB 1; Length 296;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
Db      247 ADWS 250

RESULT 47
DHMA_CAUCR
ID  DHMA CAUCR  STANDARD;      PRT;      302 AA.
AC  Q9A919;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Haloalkane dehalogenase (EC 3.8.1.5).
OS  Rattus norvegicus (Rat).
GN  DHMA OR CC1175.
OC  Caulobacter crescentus.
OC  Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC  Caulobacteraceae; Caulobacter.
OX  NCBI_TaxID=155892;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 19089 / CB15;
RX  MEDLINE=21173698; PubMed=11259647;
RA  Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA  Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA  Deocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA  DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA  Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA  Ueterbach T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA  Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT  "Complete genome sequence of Caulobacter crescentus.";
RL  Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC  -1- FUNCTION: Catalyzes hydrolytic cleavage of carbon-halogen bonds in
CC  halogenated aliphatic compounds, leading to the formation of the
CC  corresponding primary alcohols, halide ions and protons (By
CC  similarity).
CC  -1- CATALYTIC ACTIVITY: 1-haloalkane + H(2)O = a primary alcohol +
CC  halide.
CC  -1- SUBUNIT: Monomer (By similarity).
CC  -1- SIMILARITY: Belongs to the haloalkane dehalogenase family.
CC  Subfamily 1.
CC  -----
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CC  -----
CC  EMBL: AE005795; AAK23159.1; -.
DR  HSP; C87395; C87395.
DR  HSP; P22643; 1BEZ.
DR  TIGR; CC1175; -.
DR  HAMAP; MF 01230; -.
DR  InterPro; IPR000073; A/b_hydrolase.
DR  InterPro; IPR003089; AB_hydrolase.
DR  InterPro; IPR000639; Epox_hydrolase.
DR  InterPro; IPR000379; Ser_estrs.
DR  Pfam; PF00561; abhydrolase; 1.
DR  PRINTS; PR00111; ABHYDROLASE.
DR  PRINTS; PR00412; EPOXYHYDROLASE.
KW  Hydrolase; Complete proteome.
FT  ACT_SITE 123 123      NUCLEOPHILE (BY SIMILARITY).
FT  ACT_SITE 249 249      ACID (BY SIMILARITY).
FT  ACT_SITE 278 278      BASE (BY SIMILARITY).
SQ  SEQUENCE 302 AA; 33155 MW; B0B8C27EE8D9A97C CRC64;

Query Match      66.7%; Score 4; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
Db      15 ADWS 18

RESULT 48
NXP4_RAT
ID  NXP4 RAT  STANDARD;      PRT;      304 AA.
AC  Q92N4;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Neurexophilin 4 precursor.
GN  NXP4 OR NPH4.
OS  Rattus norvegicus (Rat).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=98237742; PubMed=9570794;
RA Misler M., Suedhof T.C.;
RT "Neuroxophilins form a conserved family of neuropeptide-like
RL J. Mol. Neurosci. 18:3630-3638(1998).
CC -1- FUNCTION: May be signaling molecules that resemble neuropeptides
CC and that act by binding to alpha-neurexins and possibly other
CC receptors (potential).
CC -1- SUBCELLULAR LOCATION: Secreted (potential).
CC -1- TISSUE SPECIFICITY: Brain and kidney.
CC -1- PFM: May be proteolytically processed in neuron-like cells (by
CC similarity).
CC -1- SIMILARITY: Belongs to the neuroxophilin family.
CC
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CC
DR EMBL; AF042714; AAD02227.1; -.
KW Glycoprotein; Signal.
FT SIGNAL 1 23
FT CHAIN 24 304
FT DOMAIN 24 84
FT DOMAIN 85 163
FT DOMAIN 164 220
FT DOMAIN 221 304
FT CARBOHYD 72 72
FT CARBOHYD 133 133
FT CARBOHYD 143 143
FT CARBOHYD 149 149
SQ SEQUENCE 304 AA; 32945 MW; AD2B30B351DEB4D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 304;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 65 WSWA 68

RESULT 49
CRTE ERWHE STANDARD; PRT; 307 AA.
ID -CRTE ERWHE STANDARD; PRT; 307 AA.
AC P22873;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Geranylgeranyl pyrophosphate synthetase (EC 2.5.1.29) (GGPP
DE synthetase) [Farnesyltransferase].
GN CRTE.
OS Erwinia herbicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pantoea.
OX NCBI_TaxID=549;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ERO10;
RA Armstrong G.A., Alberti M., Hearst J.E.;
RT "Conserved enzymes mediate the early reactions of carotenoid
RT biosynthesis in nonphotosynthetic and photosynthetic prokaryotes.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9975-9979(1990).
```

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RN FUNCTION.
RP MEDLINE=92357711; PubMed=1495965;
RX Math S.K., Hearst J.E., Poulter C.D.;
RT "The crte gene in Erwinia herbicola encodes geranylgeranyl
RT diphosphate synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6761-6764(1992).
CC -1- CATALYTIC ACTIVITY: trans-trans-farnesyl diphosphate + isopentenyl
CC diphosphate = diphosphate + geranylgeranyl diphosphate.
CC -1- PATHWAY: Carotenoid biosynthesis.
CC -1- SIMILARITY: Belongs to the PPP/GGPP synthetase family.
CC
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CC
DR EMBL; M89424; AAA24819.1; -.
DR EMBL; M87280; AAA64977.1; -.
DR PIR; C39273; C39273.
DR InterPro; IPR000092; Polyprenyl synt.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF00348; polyprenyl synt; 1.
DR PROSITE; PS00444; POLYPRENYL SYNTHET 2; 1.
DR PROSITE; PS00723; POLYPRENYL SYNTHET 1; 1.
KW Carotenoid biosynthesis; Isoprene biosynthesis; Transferase.
SQ SEQUENCE 307 AA; 33242 MW; 6A534C6194CE9F59 CRC64;

Query Match 66.7%; Score 4; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 298 ADWS 301

RESULT 50
NXP4_HUMAN STANDARD; PRT; 308 AA.
ID NXP4_HUMAN STANDARD; PRT; 308 AA.
AC Q95158; Q9N462;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurexophilin 4 precursor.
GN NXP4 OR NPH4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haehle F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Walek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
```

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RX [2]
RY SEQUENCE OF 225-308 FROM N.A.
RX MEDLINE=98237742; PubMed=9570794;
RA Missler M., Suedhof T.C.;
RT "Neurexophilins form a conserved family of neuropeptide-like
RL glycoproteins.";
RJ J. Mol. Neurosci. 18:3630-3638(1998).
CC -!- FUNCTION: May be signaling molecules that resemble neuropeptides
CC and that act by binding to alpha-neurexins and possibly other
CC receptors (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Expressed in brain, spleen, and testis.
CC -!- PTM: May be proteolytically processed at the boundary between the
CC N-terminal nonconserved and the central conserved domain in
CC neuron-like cells (By similarity).
CC -!- SIMILARITY: Belongs to the neurexophilin family.
CC -----
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CC -----
DR EMBL: BC036679; AAH36679.1; -.
DR EMBL: AF043469; AAD02282.1; -.
DR Genew; HGNC:8078; NXP4.
DR MIM; 604637; -.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; NAS.
KW Glycoprotein; Repeat; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 308 NEUREXOPHILIN 4.
FT DOMAIN 24 84 II.
FT DOMAIN 85 163 III.
FT DOMAIN 164 224 IV (LINKER DOMAIN).
FT DOMAIN 225 308 V (CYS-RICH).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 226 227 KE -> RG (IN REF. 2).
FT CONFLICT 296 296 Q -> P (IN REF. 2).
SQ SEQUENCE 308 AA; 33110 MW; C34C80A422316F6D CRC64;

Query Match 66.7%; Score 4; DB 1; Length 308;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
|||
Db 65 WSWA 68

Search completed: July 23, 2004, 13:27:23
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:24:25 ; Search time 16 Seconds
(without alignments)
36.072 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADMSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 78:*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	83.3	374	2 B83241	conserved hypotchet
2	5	83.3	889	2 E87304	TonB-dependent rec
3	4	66.7	32	2 A24047	gap junction prote
4	4	66.7	37	2 A59401	delta-palutrl - Pa
5	4	66.7	57	2 A23202	hypothetical prote
6	4	66.7	88	2 H95051	hypothetical prote
7	4	66.7	88	2 D97922	hypothetical prote
8	4	66.7	94	2 T10250	lectin homolog 2 -
9	4	66.7	95	2 T36897	probable xylanase
10	4	66.7	97	2 E53374	type IV prepilin p
11	4	66.7	98	2 D53374	type IV prepilin p
12	4	66.7	100	2 H81042	hypothetical prote
13	4	66.7	115	2 T31781	hypothetical prote
14	4	66.7	118	2 E30828	probable terminase
15	4	66.7	118	2 B95686	unknown protein (M
16	4	66.7	122	2 S69909	Ig V-D-J region (M
17	4	66.7	129	1 E89973	hypothetical prote
18	4	66.7	129	2 F69902	conserved hypotchet
19	4	66.7	132	2 S65785	mel-13a protein -
20	4	66.7	133	2 S70967	bfpG protein - Esc
21	4	66.7	133	2 F84190	hypothetical prote
22	4	66.7	134	2 AC2926	conserved hypotchet
23	4	66.7	134	2 H98355	hypothetical prote
24	4	66.7	135	2 B83440	hypothetical prote
25	4	66.7	137	2 G84174	Ig mu heavy chain
26	4	66.7	139	2 S54229	pathogenesis-relat
27	4	66.7	140	2 A33155	hypothetical prote
28	4	66.7	143	2 T16896	gene 29 protein -
29	4	66.7	147	2 S30974	

30	4	66.7	147	2 C72803	gp29 protein - Myc
31	4	66.7	151	2 A81863	hypothetical prote
32	4	66.7	152	2 A13271	acetyltransferase
33	4	66.7	153	2 B71131	hypothetical prote
34	4	66.7	161	2 A97671	hypothetical prote
35	4	66.7	163	2 T02054	pathogenesis relat
36	4	66.7	166	2 AE0773	conserved hypotchet
37	4	66.7	169	1 A35209	cytochrome-c oxida
38	4	66.7	169	1 S12442	ATP synthase delta
39	4	66.7	178	2 F82952	hypothetical prote
40	4	66.7	180	2 H83256	50S ribosomal prot
41	4	66.7	183	2 G84323	hypothetical prote
42	4	66.7	185	2 T28707	hypothetical prote
43	4	66.7	188	2 F95944	hypothetical prote
44	4	66.7	190	2 AC0619	hypothetical bacte
45	4	66.7	191	2 H69387	conserved hypotchet
46	4	66.7	194	2 G87453	RNA polymerase sig
47	4	66.7	196	2 G87510	hypothetical prote
48	4	66.7	197	2 E70423	conserved hypotchet
49	4	66.7	197	2 G95219	HAM1 protein [impo
50	4	66.7	200	2 T35699	probable sigma fac
51	4	66.7	203	2 D70150	hypothetical prote
52	4	66.7	203	2 E70150	hypothetical prote
53	4	66.7	205	2 G83218	heme acquisition p
54	4	66.7	206	2 C82583	RNA polymerase sig
55	4	66.7	206	2 E83047	hypothetical prote
56	4	66.7	207	2 T03331	gene e36 protein -
57	4	66.7	210	2 A87523	thiol-disulfide in
58	4	66.7	210	2 T26154	hypothetical prote
59	4	66.7	211	2 T03355	gene e12 protein -
60	4	66.7	214	2 G83692	hypothetical prote
61	4	66.7	214	2 AC1057	probable membrane
62	4	66.7	217	2 T17475	enoyl-coa hydratase
63	4	66.7	233	2 G83548	DNA repair protein
64	4	66.7	234	2 T36162	probable integral
65	4	66.7	237	2 AC1316	2-heptaprenyl-1,4-
66	4	66.7	237	2 AC1688	2-heptaprenyl-1,4-
67	4	66.7	239	2 G87550	conserved hypotchet
68	4	66.7	240	2 AH3566	hypothetical prote
69	4	66.7	240	2 F82790	GMP synthase XF056
70	4	66.7	241	2 F97752	tolQ protein [impo
71	4	66.7	243	2 E81080	conserved hypotchet
72	4	66.7	243	2 AC3600	cellulase (EC 3.2.
73	4	66.7	246	2 T33965	hypothetical prote
74	4	66.7	247	2 E95207	conserved hypotchet
75	4	66.7	251	2 E98072	conserved hypotchet
76	4	66.7	255	1 UYPV21	noncapsid protein
77	4	66.7	255	2 D69255	GDP-D-mannose dehy
78	4	66.7	257	2 D87152	conserved hypotchet
79	4	66.7	260	2 D83490	probable transcrip
80	4	66.7	261	2 S76510	hypothetical prote
81	4	66.7	262	2 C84800	3-oxo-5-alpha-ater
82	4	66.7	263	2 C87317	hypothetical prote
83	4	66.7	266	2 T35449	hypothetical prote
84	4	66.7	266	2 T15066	hypothetical prote
85	4	66.7	266	2 T29900	hypothetical prote
86	4	66.7	272	1 CCQF1R	ubiquinol-cytochro
87	4	66.7	273	2 B81211	2,3,4,5-tetrahydro
88	4	66.7	273	2 F81787	2,3,4,5-tetrahydro
89	4	66.7	275	2 T05822	hypothetical prote
90	4	66.7	276	2 H86922	probable ABC trans
91	4	66.7	276	2 D82848	hypothetical prote
92	4	66.7	276	2 D82661	hypothetical prote
93	4	66.7	277	2 AD7539	MGCI873 protein ho
94	4	66.7	277	2 A27558	esterase D (import
95	4	66.7	278	2 S75883	hypothetical prote
96	4	66.7	280	2 H83623	probable chemotaxi
97	4	66.7	280	2 C70696	probable transport
98	4	66.7	280	2 ABE2031	gamma-tocopherol m
99	4	66.7	282	1 DGEQMA	DNA-3-methyladenin
100	4	66.7	282	2 E90988	3-methyl-adenine D
101	4	66.7	282	2 G85833	3-methyl-adenine D
102	4	66.7	284	1 JC4040	transcription init

103	4	66.7	284	2	JC7148	heat-shock sigma f	176	4	66.7	365	2	S61636	hypothetical prote
104	4	66.7	286	2	D83762	transcription regu	177	4	66.7	371	2	A69421	hydrogenase expres
105	4	66.7	289	2	A10770	DNA-3-methyladenin	178	4	66.7	372	2	S74532	hypothetical prote
106	4	66.7	289	2	S38806	porin opna - Rhodo	179	4	66.7	373	2	T34743	hypothetical prote
107	4	66.7	291	1	CP8528	cytochrome c552 pr	180	4	66.7	374	2	G70947	hypothetical prote
108	4	66.7	292	2	D95921	conserved hypoteth	181	4	66.7	375	2	S50228	PAS7 protein - yea
109	4	66.7	293	2	F87457	conserved hypoteth	182	4	66.7	380	2	AH0781	probable membrane
110	4	66.7	294	2	D82371	probable polynucle	183	4	66.7	383	2	B83205	hypothetical prote
111	4	66.7	295	1	S42405	ribosomal protein	184	4	66.7	390	2	A87274	hypothetical prote
112	4	66.7	295	2	A29395	ribosomal protein	185	4	66.7	390	2	F84196	hypothetical prote
113	4	66.7	295	2	S33438	laminin receptor,	186	4	66.7	394	2	JQ1399	phosphoglycerate k
114	4	66.7	295	2	A38464	33k laminin recept	187	4	66.7	394	2	D75256	queuine tRNA ribos
115	4	66.7	295	2	A31233	ribosomal protein	188	4	66.7	395	2	A13402	salicylate 1-mono
116	4	66.7	295	4	JC6530	laminin receptor p	189	4	66.7	399	2	AD1808	hypothetical prote
117	4	66.7	297	1	S49348	cytochrome-c oxida	190	4	66.7	400	2	A49147	bone morphogenetic
118	4	66.7	298	2	F87376	hypothetical prote	191	4	66.7	400	2	AF2107	hypothetical prote
119	4	66.7	299	2	D86199	hypothetical prote	192	4	66.7	401	2	S44666	ZK370.5 protein -
120	4	66.7	300	2	I40425	carboxylesterase (193	4	66.7	401	2	JH0689	bone morphogenetic
121	4	66.7	300	2	C69664	carboxylesterase N	194	4	66.7	403	2	T33198	hypothetical prote
122	4	66.7	300	2	G87711	ada regulatory pro	195	4	66.7	404	2	D70977	hypothetical prote
123	4	66.7	302	2	C87395	haloalkane dehalog	196	4	66.7	405	2	T22675	hypothetical prote
124	4	66.7	302	2	E83589	probable transcrip	197	4	66.7	409	1	A47527	transcription fact
125	4	66.7	303	2	T47356	hypothetical prote	198	4	66.7	409	2	T47298	probable replicati
126	4	66.7	304	2	T25337	hypothetical prote	199	4	66.7	411	2	G89074	protein K04A8.5 [l
127	4	66.7	306	2	S19997	hypothetical prote	200	4	66.7	411	2	B84949	tetrahydrofolylpol
128	4	66.7	307	2	AE3284	high-affinity bran	201	4	66.7	411	2	AG3003	conserved hypoteth
129	4	66.7	308	2	C39273	phytoene synthase	202	4	66.7	411	2	B98280	hypothetical prote
130	4	66.7	310	2	T01266	starch synthase DU	203	4	66.7	415	2	AE1844	hypothetical prote
131	4	66.7	310	2	JC7853	L-fucose-specific	204	4	66.7	415	2	G84538	hypothetical prote
132	4	66.7	317	2	B72216	endoglucanase - Th	205	4	66.7	416	1	JN0006	nerve growth facto
133	4	66.7	317	2	S76618	hypothetical prote	206	4	66.7	419	2	D72357	hypothetical prote
134	4	66.7	319	2	G71284	probable methionyl	207	4	66.7	421	2	T31787	hypothetical prote
135	4	66.7	319	2	T18245	conserved hypoteth	208	4	66.7	424	2	AI0465	probable glycerol-
136	4	66.7	321	2	AG3131	dihydrodipicolinat	209	4	66.7	429	2	B87039	conserved hypoteth
137	4	66.7	321	2	D98156	probable dihydrodi	210	4	66.7	435	2	T36780	hypothetical prote
138	4	66.7	324	2	AB3548	vegetative incom	211	4	66.7	438	2	D70528	hypothetical prote
139	4	66.7	325	2	T32282	hypothetical prote	212	4	66.7	439	2	T52321	taxadienol acetyl
140	4	66.7	328	2	E72424	oligopeptide ABC t	213	4	66.7	441	2	F84560	purple acid phosph
141	4	66.7	328	2	I39492	NifR3 protein - Az	214	4	66.7	443	2	T35974	probable aminoacyl
142	4	66.7	330	2	B96027	probable aliphatic	215	4	66.7	445	2	S27492	hypothetical prote
143	4	66.7	334	2	T36052	probable cytochrom	216	4	66.7	445	2	E82075	hypothetical prote
144	4	66.7	336	2	E98083	hypothetical prote	217	4	66.7	449	2	H70546	hypothetical prote
145	4	66.7	337	2	T22570	hypothetical prote	218	4	66.7	450	2	B70506	hypothetical prote
146	4	66.7	338	2	S75196	hypothetical prote	219	4	66.7	452	2	H91172	probable phosphotr
147	4	66.7	338	2	C75338	conserved hypoteth	220	4	66.7	452	2	AH0964	probable PTS syste
148	4	66.7	338	2	E91190	probable regulator	221	4	66.7	452	2	T33248	hypothetical prote
149	4	66.7	338	2	F86037	probable regulator	222	4	66.7	453	1	NMIV3	exo-alpha-sialidas
150	4	66.7	339	2	T22571	hypothetical prote	223	4	66.7	454	1	NMIV	exo-alpha-sialidas
151	4	66.7	340	2	H82812	conserved hypoteth	224	4	66.7	457	2	AB2657	glutamate-cysteine
152	4	66.7	342	2	AD3197	citrate synthase [225	4	66.7	457	2	G97438	probable replicati
153	4	66.7	344	2	H70030	conserved hypoteth	226	4	66.7	458	2	A84487	oxygen-independent
154	4	66.7	344	2	E84526	probable lysosomal	227	4	66.7	460	2	A83454	hypothetical prote
155	4	66.7	345	2	AG3401	porphobilinogen sy	228	4	66.7	462	2	H86018	hypothetical prote
156	4	66.7	346	1	BYECPR	phosphate-repressi	229	4	66.7	463	2	F81194	hypothetical prote
157	4	66.7	346	2	H91211	phosphate-binding	230	4	66.7	463	2	E81830	hypothetical prote
158	4	66.7	346	2	H86057	phosphate-binding	231	4	66.7	464	2	AG1146	beta-glucosidase h
159	4	66.7	346	2	AB0956	periplasmic phosph	232	4	66.7	464	2	AG1505	beta-glucosidase h
160	4	66.7	347	1	S01340	D-amino-acid oxida	233	4	66.7	464	2	S75362	hypothetical prote
161	4	66.7	347	1	JX0132	D-amino-acid oxida	234	4	66.7	466	2	F84139	beta-glucosidase B
162	4	66.7	347	2	H87715	ferrochelatase lim	235	4	66.7	467	2	AC3324	UDP-N-acetylmuram
163	4	66.7	347	2	D69373	immunogenic protei	236	4	66.7	467	2	H84538	hypothetical prote
164	4	66.7	348	2	C96673	gamma-tocopherol m	237	4	66.7	471	2	E56146	cpdB protein homol
165	4	66.7	351	2	S11519	phosphatidylcholin	238	4	66.7	471	2	I41251	GDP-mannose pyroph
166	4	66.7	354	2	G86251	protein F25C20.6 [239	4	66.7	471	2	I84556	GDP-manno pyrophos
167	4	66.7	354	2	G83134	polyamine transpor	240	4	66.7	471	2	I57096	mannose-1-phosphat
168	4	66.7	360	2	T26037	hypothetical prote	241	4	66.7	471	2	C87566	UDP-N-acetylmuram
169	4	66.7	360	2	S32695	Wnt-2 protein - Ca	242	4	66.7	474	2	T38485	centromere/microtu
170	4	66.7	360	2	S60888	ferric exochelin b	243	4	66.7	476	2	AG1051	probable transport
171	4	66.7	361	2	S77525	hypothetical prote	244	4	66.7	477	2	S77373	hypothetical prote
172	4	66.7	362	2	S23471	uroporphyrinogen d	245	4	66.7	477	2	H95936	probable nucleotid
173	4	66.7	363	2	A29072	pulmonary surfacta	246	4	66.7	483	2	H90210	hypothetical prote
174	4	66.7	364	2	G82595	ABC transporter ph	247	4	66.7	484	2	A86116	hypothetical prote
175	4	66.7	364	2	S76068	hypothetical prote	248	4	66.7	484	2	D65230	hypothetical 52.9

249	4	66.7	484	2	A98275	hypothetical prote	322	4	66.7	714	2	A82366	hypothetical prote
250	4	66.7	487	2	F70765	hypothetical prote	323	4	66.7	715	2	S70397	zona pellucida gly
251	4	66.7	489	2	C70655	probable monooxyge	324	4	66.7	716	2	S70398	zona pellucida gly
252	4	66.7	491	2	D84967	glucose-6-phosphat	325	4	66.7	720	2	A36942	Fe(III)-pyochelin
253	4	66.7	491	2	F83383	probable flavin-bi	326	4	66.7	726	2	D97012	probable processiv
254	4	66.7	494	2	A86917	probable monooxyge	327	4	66.7	730	2	E87251	isoquinoline 1-oxi
255	4	66.7	498	2	A87374	hypothetical prote	328	4	66.7	730	2	S37384	catalase (EC 1.11.
256	4	66.7	501	2	G72206	GMP synthase - The	329	4	66.7	730	2	S48813	hypothetical prote
257	4	66.7	507	2	AH2717	exopolysphosphate	330	4	66.7	731	2	A83410	probable oxidoredu
258	4	66.7	507	2	C97499	guanosine-5'-triph	331	4	66.7	739	2	S15727	cellulase (EC 3.2.
259	4	66.7	516	2	T02189	hypothetical prote	332	4	66.7	745	1	I49101	conserved helix-lo
260	4	66.7	527	2	T33175	hypothetical prote	333	4	66.7	747	2	D70802	hypothetical prote
261	4	66.7	527	2	T21830	hypothetical prote	334	4	66.7	756	2	T49475	related to tol pro
262	4	66.7	532	2	G83424	hypothetical prote	335	4	66.7	757	2	D95103	X-pro dipeptidyl-p
263	4	66.7	534	2	S76219	hypothetical prote	336	4	66.7	758	2	T48815	mixed-linked glucu
264	4	66.7	534	2	D42463	hypothetical prote	337	4	66.7	766	2	T03218	armadillo-like pro
265	4	66.7	536	2	F70597	hypothetical prote	338	4	66.7	766	2	A86198	hypothetical prote
266	4	66.7	537	2	T06728	pectate lyase (EC	339	4	66.7	768	2	T51209	related to tol pro
267	4	66.7	542	2	JC4812	hyaluronan synthas	340	4	66.7	771	2	A83348	probable aldehyde
268	4	66.7	543	2	S52081	diphosphate-fructo	341	4	66.7	773	2	TU0135	aldehyde dehydroge
269	4	66.7	544	2	T27614	hypothetical prote	342	4	66.7	783	2	JC6136	kelxin-like protein
270	4	66.7	545	2	AB3150	fatty acid CoA lig	343	4	66.7	786	2	E87565	conserved hypochet
271	4	66.7	546	2	G98137	hypothetical prote	344	4	66.7	787	2	T49614	related to tol pro
272	4	66.7	547	1	A32244	60K cysteine-rich	345	4	66.7	795	2	B97971	x-pro dipeptidyl-p
273	4	66.7	547	2	B43584	60K cysteine-rich	346	4	66.7	802	2	A83125	probable TonB-depe
274	4	66.7	548	2	H75632	Na(+)-linked D-ala	347	4	66.7	803	2	F90485	hypothetical prote
275	4	66.7	548	2	B84306	hypothetical prote	348	4	66.7	810	2	S44653	F42H10.5 protein -
276	4	66.7	550	1	VGBE18	glycoprotein E - h	349	4	66.7	813	2	T04220	H+-transporting AT
277	4	66.7	553	2	D71515	60K cysteine-rich	350	4	66.7	834	2	S66258	glucosidase I - hu
278	4	66.7	553	2	T06089	hypothetical prote	351	4	66.7	836	2	D87084	phenylalanyl-tRNA
279	4	66.7	553	2	AC0085	conserved hypochet	352	4	66.7	836	2	T30312	pin biosynthetic
280	4	66.7	554	2	C81671	60 kDa outer membr	353	4	66.7	836	2	D82177	conserved hypochet
281	4	66.7	556	1	S12602	60K cysteine-rich	354	4	66.7	848	2	E95092	aminopeptidase N (
282	4	66.7	556	2	A86560	60 kDa Cysteine-ri	355	4	66.7	848	2	B97960	conserved hypochet
283	4	66.7	556	2	A69718	squalene-hopene cy	356	4	66.7	862	2	H82182	conserved hypochet
284	4	66.7	557	1	B39439	60K cysteine-rich	357	4	66.7	883	2	C83385	hypothetical prote
285	4	66.7	567	2	AF0308	menaquinone biosyn	358	4	66.7	884	2	S77031	hypothetical prote
286	4	66.7	567	2	T43555	Ras pathway intera	359	4	66.7	895	2	A55514	pyruvate dehydroge
287	4	66.7	567	2	E91095	type III secretion	360	4	66.7	909	2	AG3419	phage host specif
288	4	66.7	567	2	A85941	type III secretion	361	4	66.7	911	2	T08108	nitrate reductase
289	4	66.7	570	2	A11828	flavoprotein [impo	362	4	66.7	915	2	A43802	cellulase (EC 3.2.
290	4	66.7	587	2	A10180	conserved hypochet	363	4	66.7	915	2	A83109	isoleucine-tRNA li
291	4	66.7	589	2	AC3334	metal chelate oute	364	4	66.7	917	2	T50379	related to tol pro
292	4	66.7	601	1	A64222	heat shock protein	365	4	66.7	917	2	B81309	hypothetical colle
293	4	66.7	602	1	T35760	2',3'-cyclic-nucle	366	4	66.7	929	2	T38948	probable oxidoredu
294	4	66.7	602	2	AB2313	hypothetical prote	367	4	66.7	943	2	B83068	probable oxidoredu
295	4	66.7	608	2	S09790	hypothetical prote	368	4	66.7	946	2	F84280	ATP-dependent heli
296	4	66.7	609	2	H90398	hypothetical prote	369	4	66.7	975	2	B34751	hypothetical prote
297	4	66.7	613	2	AH2398	hypothetical prote	370	4	66.7	983	2	B45583	receptor tyrosine
298	4	66.7	626	2	T08686	intracellular prot	371	4	66.7	983	2	A38224	protein-tyrosine k
299	4	66.7	627	2	H86180	hypothetical prote	372	4	66.7	983	2	A45583	receptor tyrosine
300	4	66.7	629	2	B95299	probable Cyaf4 ade	373	4	66.7	989	2	T46183	zinc proteinase (E
301	4	66.7	630	1	G64226	hypothetical prote	374	4	66.7	994	2	B82843	valyl-tRNA synthet
302	4	66.7	637	2	T26593	hypothetical prote	375	4	66.7	1011	2	T17430	tol protein - Neur
303	4	66.7	643	2	E83142	probable transcrip	376	4	66.7	1018	2	T40253	hypothetical prote
304	4	66.7	648	2	A48646	amine oxidase (cop	377	4	66.7	1019	2	A83613	conserved hypochet
305	4	66.7	654	2	AG7517	acetyl/propionyl-C	378	4	66.7	1025	2	H86250	hypothetical prote
306	4	66.7	654	2	C83522	iron-regulated out	379	4	66.7	1028	2	T03516	probable outer mem
307	4	66.7	655	2	A12556	hypothetical prote	380	4	66.7	1035	2	T42093	phospholipase D (E
308	4	66.7	657	2	G33906	hypothetical prote	381	4	66.7	1036	2	T13732	phospholipase D (E
309	4	66.7	665	2	AD0160	probable outer mem	382	4	66.7	1036	2	T18530	phospholipase D (E
310	4	66.7	665	2	F86181	protein F13W7.17 [383	4	66.7	1037	2	T13943	phospholipase D (E
311	4	66.7	678	2	T13773	NADH2 dehydrogenas	384	4	66.7	1039	2	T28644	cellulase (EC 3.2.
312	4	66.7	678	2	A75580	hypothetical prote	385	4	66.7	1039	2	S02711	cellulase (EC 3.2.
313	4	66.7	679	2	AC0333	probable membrane	386	4	66.7	1052	1	A44937	kinetoplast-associ
314	4	66.7	683	2	D82674	TonB-dependent rec	387	4	66.7	1057	1	OYRTR	atrial natriuretic
315	4	66.7	689	2	T52060	protein MEDA (imp	388	4	66.7	1057	1	OYMSAR	natriuretic peptid
316	4	66.7	692	2	S37976	hypothetical prote	389	4	66.7	1057	2	I57963	guanylyl cyclase A
317	4	66.7	698	2	S52671	general sporulation	390	4	66.7	1057	2	I55319	natriuretic peptid
318	4	66.7	699	2	AG0371	probable acetyltra	391	4	66.7	1061	1	OYHUAR	natriuretic peptid
319	4	66.7	700	2	B41897	cellulase (EC 3.2.	392	4	66.7	1074	2	T17203	phospholipase D (E
320	4	66.7	705	2	A35621	spore germination pr	393	4	66.7	1074	2	T13725	phospholipase D (E
321	4	66.7	707	2	S77094	glycogen operon pr	394	4	66.7	1075	2	T46635	phospholipase D (E

395	4	66.7	1097	2	S17308	leukemia inhibitor	468	3	50.0	37	1	E32038	mu-agatoxin V - fu
396	4	66.7	1105	2	A71430	hypothetical prote	469	3	50.0	37	1	F32038	mu-agatoxin VI - f
397	4	66.7	1107	1	JQ1658	genome polyprotein	470	3	50.0	37	1	B32038	mu-agatoxin II - f
398	4	66.7	1125	2	T39052	hypothetical serin	471	3	50.0	37	2	T11961	hypothetical prote
399	4	66.7	1139	2	A10379	probable potassium	472	3	50.0	37	2	E97596	hypothetical prote
400	4	66.7	1147	2	D87295	smc protein [impor	473	3	50.0	38	1	B35030	curtatoxin II - fu
401	4	66.7	1215	2	C84848	hypothetical prote	474	3	50.0	38	1	C32038	mu-agatoxin III -
402	4	66.7	1230	2	T07663	soluble starch syn	475	3	50.0	38	1	C35030	curtatoxin III - f
403	4	66.7	1245	2	E83110	exodeoxyribonuclea	476	3	50.0	39	2	S26937	ig heavy chain v f
404	4	66.7	1259	2	H65233	ycf1n protein - Esc	477	3	50.0	39	2	S77904	tax protein - siml
405	4	66.7	1259	2	G91278	hypothetical prote	478	3	50.0	40	2	A43853	fructose-bisphosph
406	4	66.7	1259	2	G86119	hypothetical prote	479	3	50.0	40	2	B58829	alboagregin-B alp
407	4	66.7	1259	2	A21055	hypothetical prote	480	3	50.0	40	2	A82382	hypothetical prote
408	4	66.7	1266	2	A26295	conserved hypothet	481	3	50.0	40	2	C69400	hypothetical prote
409	4	66.7	1266	2	G37477	hypothetical prote	482	3	50.0	40	2	A56829	alboagregin-B bet
410	4	66.7	1271	2	T49009	protein kinase lik	483	3	50.0	40	2	S56007	tokaracetin beta c
411	4	66.7	1329	2	D87226	conserved hypothet	484	3	50.0	40	2	C97353	probable membrane
412	4	66.7	1329	2	A72647	probable surface l	485	3	50.0	40	2	C30518	ig heavy chain V-A
413	4	66.7	1331	2	A48954	mannan endo-1,4-be	486	3	50.0	43	2	C41397	hypothetical prote
414	4	66.7	1334	2	T50568	probable multi-dom	487	3	50.0	43	2	H82619	hypothetical prote
415	4	66.7	1366	2	C85077	probable polyprote	488	3	50.0	44	2	E95248	hypothetical prote
416	4	66.7	1423	2	A49206	exo-beta-D-fructos	489	3	50.0	45	2	S36709	B7 protein - equin
417	4	66.7	1558	2	A82457	two-component hybr	490	3	50.0	48	2	I79271	trans protein - Esc
418	4	66.7	1573	2	T50113	3-dehydroquinase s	491	3	50.0	49	2	PL0163	lysozyme (EC 3.2.1
419	4	66.7	1616	1	JQ2144	183K protein - tom	492	3	50.0	50	2	D90403	hypothetical prote
420	4	66.7	1674	2	T01265	starch synthase DU	493	3	50.0	50	2	H90542	hypothetical prote
421	4	66.7	1711	2	T31337	1,4-beta-glucanase	494	3	50.0	50	2	T00156	hypothetical prote
422	4	66.7	1742	2	T17120	cellulase (EC 3.2.	495	3	50.0	51	2	S00576	hypothetical prote
423	4	66.7	1779	2	T31085	xylanase - Caldica	496	3	50.0	51	2	F82846	hypothetical prote
424	4	66.7	1937	2	T03224	probable polyketid	497	3	50.0	52	1	AB1954	rubredoxin - Desul
425	4	66.7	1979	1	S03166	myosin heavy chain	498	3	50.0	52	1	RUDV	rubredoxin - Megal
426	4	66.7	2472	2	E83594	still frameshift p	499	3	50.0	52	1	JX0241	rubredoxin - Helio
427	4	66.7	2559	2	T09144	probable guanine n	500	3	50.0	52	1	RUMB	variant surface gl
428	4	66.7	3005	2	T08841	polyprotein - dour	501	3	50.0	52	2	S65620	gene 87 protein -
429	4	66.7	3161	2	T30342	protein HWPI - Ye	502	3	50.0	52	2	B21440	hypothetical prote
430	4	66.7	3163	2	T17440	probable polyketid	503	3	50.0	53	2	S31032	hypothetical prote
431	4	66.7	3163	2	AB0233	yersiniabactin bio	504	3	50.0	53	2	A82960	hypothetical prote
432	4	66.7	3175	1	RWRVE6	genome polyprotein	505	3	50.0	53	2	A22338	beta-2-microglobul
433	4	66.7	3421	1	W2BEB6	367K tegument prot	506	3	50.0	54	2	S15757	SOX-11 protein - A
434	4	66.7	3534	2	T42567	tegument protein 2	507	3	50.0	54	2	S22946	gp87 protein - Myc
435	4	66.7	3670	2	T36249	CDA peptide synthe	508	3	50.0	54	2	D82733	hypothetical prote
436	4	66.7	3670	2	G70944	probable polyketid	509	3	50.0	54	2	A29225	transposase tnp [i
437	3	50.0	7	2	PT0688	T-cell receptor be	510	3	50.0	54	2	H82976	rubredoxin PA5350
438	3	50.0	8	2	PT0724	T-cell receptor be	511	3	50.0	55	2	T11171	H+-transporting tw
439	3	50.0	9	2	I58350	gene c-mpl protein	512	3	50.0	55	2	E90614	ATP synthase F0 ch
440	3	50.0	10	2	A59272	peptide-N4-(N-acet	513	3	50.0	55	2	E90618	ATP synthase F0 ch
441	3	50.0	10	2	B38887	T-cell receptor ga	514	3	50.0	55	2	E90620	ATP synthase F0 ch
442	3	50.0	11	2	C38887	T-cell receptor ga	515	3	50.0	55	2	E90624	ATP synthase F0 ch
443	3	50.0	11	2	I41946	T-cell receptor ga	516	3	50.0	55	2	B90626	ATP synthase F0 ch
444	3	50.0	12	2	H41946	T-cell receptor ga	517	3	50.0	55	2	B46485	ig epsilon chain C
445	3	50.0	13	2	PH0928	T-cell receptor ga	518	3	50.0	55	2	A84180	hypothetical prote
446	3	50.0	14	2	S14336	mastoparan B - hor	519	3	50.0	55	2	S46977	lysis protein - ph
447	3	50.0	15	2	A49372	agarase (EC 3.2.1.	520	3	50.0	55	2	A84180	protein [imported
448	3	50.0	15	2	PH1616	benzoyl-CoA ligase	521	3	50.0	55	2	H95383	hypothetical prote
449	3	50.0	16	2	A48630	ig H chain V-D-J r	522	3	50.0	55	2	AD1852	hypothetical prote
450	3	50.0	16	2	A48630	bothrojaracin - ja	523	3	50.0	56	2	B30518	ig heavy chain V-A
451	3	50.0	17	2	S19614	globin - polychaet	524	3	50.0	56	2	S35645	homeotic protein S
452	3	50.0	20	2	S58382	hypothetical prote	525	3	50.0	56	2	S35645	sox protein - less
453	3	50.0	20	2	Q00071	T-cell receptor be	526	3	50.0	56	2	S45073	hypothetical prote
454	3	50.0	21	2	A60420	lens intrinsic mem	527	3	50.0	56	2	C82632	hypothetical prote
455	3	50.0	21	2	S03863	carbonate dehydrat	528	3	50.0	57	2	H35057	MHC class II histo
456	3	50.0	21	2	S03863	ELAV-like neuronal	529	3	50.0	57	2	T46518	hypothetical prote
457	3	50.0	24	2	I38753	pancreatic endopep	530	3	50.0	57	2	T07499	hypothetical prote
458	3	50.0	25	2	S12997	hypothetical prote	531	3	50.0	57	2	A49111	hypothetical prote
459	3	50.0	25	2	F84066	factor IX/factor X	532	3	50.0	58	2	S49347	POU homeodomain pr
460	3	50.0	30	2	B53088	factor IX/factor X	533	3	50.0	59	1	VIEPIA	gene insl protein
461	3	50.0	30	2	A53088	hypothetical prote	534	3	50.0	59	1	S49347	venom basic protei
462	3	50.0	33	2	E82391	cycochrome c6 [imp	535	3	50.0	60	2	D70593	probable rubb prot
463	3	50.0	35	2	AH1838	hypothetical prote	536	3	50.0	60	2	T19621	hypothetical prote
464	3	50.0	36	2	S73127	ycf32 protein - Od	537	3	50.0	60	2	C64860	hypothetical prote
465	3	50.0	36	2	S78239	hypothetical prote	538	3	50.0	61	2	E50515	hypothetical prote
466	3	50.0	36	2	D84275	hypothetical prote	539	3	50.0	61	2	A84615	hypothetical prote
467	3	50.0	37	1	D32038	mu-agatoxin IV - f	540	3	50.0	61	2	AC1443	hypothetical prote

541	3	50.0	61	2	AC2673	hypothetical prote	614	77	2	S35844	envelope protein -
542	3	50.0	62	2	S3002	mitotic-specific c	615	77	2	S35840	envelope protein -
543	3	50.0	62	2	D59352	depressant insect	616	77	2	S35806	envelope protein -
544	3	50.0	63	2	C42361	DNA-directed RNA p	617	77	2	S35841	envelope protein -
545	3	50.0	63	2	T12121	NADH dehydrogenase	618	77	2	S35804	envelope protein -
546	3	50.0	63	2	B98002	hypothetical prote	619	77	2	S35843	envelope protein -
547	3	50.0	63	2	AI0519	conserved hypothet	620	77	2	C82409	hypothetical prote
548	3	50.0	63	2	AI1856	hypothetical prote	621	77	2	T13007	hypothetical prote
549	3	50.0	64	1	APBP22	endopeptidase (EC	622	77	2	T01740	hypothetical prote
550	3	50.0	64	2	T16998	S-like ribonucleas	623	77	2	AI3031	hypothetical prote
551	3	50.0	64	2	G87525	transcription regu	624	77	2	B98254	hypothetical prote
552	3	50.0	64	2	AC0432	hypothetical prote	625	78	2	JK0297	alpha-amylase inh
553	3	50.0	65	1	R5BPX8	excisionase - phag	626	78	2	G30517	ig heavy chain pre
554	3	50.0	65	2	A30642	hypothetical prote	627	78	2	T32364	hypothetical prote
555	3	50.0	65	2	S74702	hypothetical prote	628	78	2	H82796	hypothetical prote
556	3	50.0	65	2	A85493	hypothetical prote	629	78	2	E82599	hypothetical prote
557	3	50.0	65	2	E64732	yacG protein - Esc	630	78	2	AG2805	hypothetical prote
558	3	50.0	66	2	P95249	conserved domain p	631	78	2	AD2028	hypothetical prote
559	3	50.0	66	2	S09855	hypothetical prote	632	79	2	I77326	NADH2 dehydrogenas
560	3	50.0	66	2	G81965	hypothetical prote	633	79	2	I77328	NADH2 dehydrogenas
561	3	50.0	66	2	C81872	hypothetical prote	634	79	2	I77324	NADH2 dehydrogenas
562	3	50.0	66	2	E81150	hypothetical prote	635	79	2	I77322	NADH2 dehydrogenas
563	3	50.0	66	2	I40095	hypothetical prote	636	79	2	F91093	type III secretion
564	3	50.0	66	2	T29847	hypothetical prote	637	79	2	B82523	hypothetical prote
565	3	50.0	66	2	C98114	hypothetical prote	638	79	2	C95852	hypothetical prote
566	3	50.0	67	2	S78325	photosystem II pho	639	79	2	AI1891	hypothetical prote
567	3	50.0	67	2	T17586	hypothetical prote	640	80	2	T31267	4-oxalocrotonoate
568	3	50.0	67	2	F72226	hypothetical prote	641	80	2	AB1932	hypothetical prote
569	3	50.0	67	2	B81975	hypothetical prote	642	80	2	AE2529	hypothetical prote
570	3	50.0	68	2	D72428	hypothetical prote	643	81	1	IHTF	high potential iro
571	3	50.0	68	2	D81806	hypothetical prote	644	81	2	D87161	hypothetical prote
572	3	50.0	68	2	S28483	ribs protein - Vib	645	81	2	G87197	hypothetical prote
573	3	50.0	68	2	E98055	hypothetical prote	646	81	2	G70534	hypothetical prote
574	3	50.0	69	1	QOECP7	ybeB protein - Esc	647	81	2	G98177	hypothetical prote
575	3	50.0	69	2	C90713	hypothetical prote	648	81	2	H97567	hypothetical prote
576	3	50.0	69	2	G95563	hypothetical prote	649	81	2	AG2488	hypothetical prote
577	3	50.0	69	2	C83914	hypothetical prote	650	82	2	I36923	gene MHC DQ-beta 1
578	3	50.0	69	2	AD1147	hypothetical prote	651	82	2	I50968	MHC class II beta
579	3	50.0	69	2	AD1506	hypothetical prote	652	82	2	I50986	MHC class II beta
580	3	50.0	70	2	I30517	ig heavy chain V-A	653	82	2	I51148	gene MHC DQ-beta 1
581	3	50.0	70	2	A30518	ig heavy chain V-A	654	82	2	I61809	core protein - hep
582	3	50.0	70	2	I49450	Zinc alpha 2 glyco	655	82	2	PQ0804	sugar transport pr
583	3	50.0	70	2	AH0102	hypothetical prote	656	82	2	T10145	sugar transport pr
584	3	50.0	71	1	N2NJIW	long neurotoxin 1	657	82	2	T10147	probable hexose tr
585	3	50.0	71	2	AE4032	hypothetical prote	658	82	2	T10131	sugar transport pr
586	3	50.0	71	2	E75316	hypothetical prote	659	82	2	T10131	sugar transport pr
587	3	50.0	71	2	B45874	ig alpha-1 chain C	660	82	2	T10146	sugar transport pr
588	3	50.0	71	2	C45874	ig alpha-2 chain C	661	82	2	T10148	thioesterase homol
589	3	50.0	72	2	T10937	cellulase (EC 3.2.	662	82	2	T09795	probable allophyc
590	3	50.0	72	2	JC2384	corazonin precursor	663	83	1	S25307	hypothetical prote
591	3	50.0	72	2	T11887	ATP synthetase sub	664	83	2	S57532	hypothetical prote
592	3	50.0	72	2	F82825	hypothetical prote	665	83	2	B72392	hypothetical prote
593	3	50.0	72	2	AD2464	hypothetical prote	666	83	2	H85762	probable transposa
594	3	50.0	72	2	T30357	hypothetical prote	667	83	2	AF2563	hypothetical prote
595	3	50.0	73	2	E42524	A-ORF-1 protein -	668	84	2	PS0142	replication-associ
596	3	50.0	73	2	S27115	probable regulator	669	84	2	F75352	hypothetical prote
597	3	50.0	73	2	F70641	hypothetical prote	670	84	2	D70596	probable whal pr
598	3	50.0	73	2	A02058	hypothetical phage	671	84	2	S12411	hypothetical prote
599	3	50.0	73	2	A83264	hypothetical prote	672	84	2	AC0301	hypothetical prote
600	3	50.0	74	2	S00166	somatostatin II pr	673	85	2	T44555	hypothetical prote
601	3	50.0	74	2	H84256	hypothetical prote	674	85	2	T35316	hypothetical prote
602	3	50.0	74	2	T32245	hypothetical prote	675	85	2	B97031	hypothetical prote
603	3	50.0	74	2	B82597	hypothetical prote	676	86	2	F34964	ig heavy chain V-1
604	3	50.0	75	2	PQ0805	core protein - hep	677	86	2	S23992	trbE protein - Esc
605	3	50.0	75	2	S11797	regB protein - pse	678	86	2	S08493	hypothetical prote
606	3	50.0	76	2	S11704	aminoglycoside 3'	679	86	2	T44923	hypothetical prote
607	3	50.0	76	2	H30517	ig heavy chain V-A	680	86	2	AG0108	hypothetical prote
608	3	50.0	76	2	H64677	hypothetical prote	681	86	2	C97474	hypothetical prote
609	3	50.0	76	2	F71838	probable nadh oxid	682	87	2	F84161	hypothetical prote
610	3	50.0	76	2	T31568	hypothetical prote	683	87	2	H84234	hypothetical prote
611	3	50.0	76	2	AC3626	hypothetical prote	684	87	2	S01071	hypothetical prote
612	3	50.0	77	1	WISMG	alpha-amylase inh	685	87	2	AF2380	hypothetical prote
613	3	50.0	77	2	S35823	envelope protein -	686	88	1	EDB551	immediate-early-5

687	3	50.0	88	2	A47760	retrovirus-related	760	3	50.0	97	2	S12416	Ig heavy chain V r
688	3	50.0	88	2	F83979	hypothetical prote	761	3	50.0	97	2	A99427	partial transposas
689	3	50.0	88	2	G97137	hypothetical prote	762	3	50.0	97	2	C56556	fork head homolog
690	3	50.0	88	2	H86125	hypothetical prote	763	3	50.0	97	2	S75011	hypothetical prote
691	3	50.0	89	2	T09494	NADPH-ferrihinopro	764	3	50.0	97	2	S72866	hypothetical prote
692	3	50.0	89	2	E84409	thioredoxin [impor	765	3	50.0	97	2	D64344	hypothetical prote
693	3	50.0	89	2	S61244	probable myristyla	766	3	50.0	97	2	S53474	hypothetical prote
694	3	50.0	89	2	A47099	hypothetical prote	767	3	50.0	97	2	A82631	hypothetical prote
695	3	50.0	89	2	T08295	hypothetical prote	768	3	50.0	97	2	G97413	hypothetical prote
696	3	50.0	89	2	T46210	hypothetical prote	769	3	50.0	97	2	B32382	beta-2-microglobul
697	3	50.0	89	2	T23831	hypothetical prote	770	3	50.0	98	1	ZNBPFE	gene N protein - p
698	3	50.0	89	2	D82601	hypothetical prote	771	3	50.0	98	2	S26904	Ig heavy chain V r
699	3	50.0	89	2	AC3452	hypothetical prote	772	3	50.0	98	2	S26905	Ig heavy chain V r
700	3	50.0	90	1	MNBPFE	major membrane pro	773	3	50.0	98	2	AG0651	conserved hypothet
701	3	50.0	90	2	A49140	glutathione transi	774	3	50.0	98	2	H64885	probable host-nucl
702	3	50.0	90	2	A65037	hypothetical 9.9 k	775	3	50.0	98	2	H91003	gp4 protein - Myco
703	3	50.0	90	2	C85905	hypothetical prote	776	3	50.0	98	2	D72800	gene 4 protein - M
704	3	50.0	90	2	E31060	hypothetical prote	777	3	50.0	98	2	S30952	hypothetical prote
705	3	50.0	90	2	D86690	hypothetical prote	778	3	50.0	98	2	T10114	hypothetical prote
706	3	50.0	90	2	G83334	hypothetical prote	779	3	50.0	98	2	F83404	hypothetical prote
707	3	50.0	90	2	C75345	hypothetical prote	780	3	50.0	98	2	T14691	hypothetical prote
708	3	50.0	90	2	S09252	hypothetical prote	781	3	50.0	98	2	F70769	hypothetical prote
709	3	50.0	91	2	A40076	cytochrome-c oxida	782	3	50.0	98	2	A85638	hypothetical prote
710	3	50.0	91	2	I51179	IGF-I receptor - c	783	3	50.0	98	2	D85848	hypothetical prote
711	3	50.0	91	2	C27578	T-cell receptor be	784	3	50.0	99	1	MGRBB2	beta-2-microglobul
712	3	50.0	91	2	C83414	hypothetical prote	785	3	50.0	99	2	S26803	Ig heavy chain V r
713	3	50.0	91	2	C43940	lactococcin B immu	786	3	50.0	99	2	S26802	Ig heavy chain V r
714	3	50.0	91	2	F89879	conserved hypothet	787	3	50.0	99	2	S26807	Ig heavy chain V r
715	3	50.0	92	2	I84730	beta-2-microglobul	788	3	50.0	99	2	S26801	Ig heavy chain V r
716	3	50.0	92	2	E90483	first ORF in trans	789	3	50.0	99	2	S28899	Ig heavy chain V r
717	3	50.0	92	2	D83065	hypothetical prote	790	3	50.0	99	2	I54312	beta 2-microglobul
718	3	50.0	92	2	T44734	hypothetical prote	791	3	50.0	99	2	S37447	hypothetical prote
719	3	50.0	92	2	C70547	hypothetical prote	792	3	50.0	99	2	S37448	gene E2 protein -
720	3	50.0	92	2	T12859	hypothetical prote	793	3	50.0	99	2	S37441	gene E2 protein -
721	3	50.0	93	1	A49205	virulence-associat	794	3	50.0	99	2	S37442	gene E2 protein -
722	3	50.0	93	2	F84175	hypothetical prote	795	3	50.0	99	2	S37444	conserved hypothet
723	3	50.0	93	2	D70963	hypothetical prote	796	3	50.0	99	2	E83244	hypothetical prote
724	3	50.0	93	2	AC2676	hypothetical prote	797	3	50.0	99	2	F91126	hypothetical prote
725	3	50.0	93	2	AE2875	conserved hypothet	798	3	50.0	99	2	T22965	hypothetical prote
726	3	50.0	93	2	B97458	hypothetical prote	799	3	50.0	99	2	E85971	conserved hypothet
727	3	50.0	93	2	AD2047	hypothetical prote	800	3	50.0	99	2	A65099	probable phage-rel
728	3	50.0	94	2	S53374	type IV prelin p	801	3	50.0	99	2	AE0895	hypothetical prote
729	3	50.0	94	2	S10948	sex-determining pr	802	3	50.0	100	2	AG0447	hypothetical prote
730	3	50.0	94	2	S75465	hypothetical prote	803	3	50.0	100	2	G89963	hypothetical prote
731	3	50.0	94	2	D70608	hypothetical prote	804	3	50.0	100	2	H72680	hypothetical prote
732	3	50.0	94	2	B70930	hypothetical prote	805	3	50.0	100	2	A10333	probable heme expo
733	3	50.0	94	2	C70662	hypothetical prote	806	3	50.0	101	2	T10066	conserved hypothet
734	3	50.0	94	2	D70560	hypothetical prote	807	3	50.0	101	2	AI0631	probable pheromone
735	3	50.0	94	2	T36982	probable insertion	808	3	50.0	101	2	A71135	hypothetical prote
736	3	50.0	94	2	B82518	hypothetical prote	809	3	50.0	101	2	D56272	hypothetical prote
737	3	50.0	95	2	I67527	CD33 antigen homol	810	3	50.0	101	2	T36592	hypothetical prote
738	3	50.0	95	2	A46422	calcium channel al	811	3	50.0	102	2	F90997	probable minor tai
739	3	50.0	95	2	E90774	hypothetical prote	812	3	50.0	102	2	E85817	probable minor homol
740	3	50.0	95	2	G90774	hypothetical prote	813	3	50.0	102	2	H64140	ybeB protein gp44 - pha
741	3	50.0	95	2	E86447	protein F5p14.5 [i	814	3	50.0	102	2	S29532	hypothetical prote
742	3	50.0	95	2	C86489	hypothetical prote	815	3	50.0	102	2	T13130	hypothetical prote
743	3	50.0	95	2	T04973	hypothetical prote	816	3	50.0	102	2	A65009	hypothetical prote
744	3	50.0	95	2	B45519	variant surface gl	817	3	50.0	102	2	T49387	ywcB protein - Bac
745	3	50.0	95	2	B85637	hypothetical prote	818	3	50.0	102	2	C96595	hypothetical prote
746	3	50.0	96	2	E69063	hypothetical prote	819	3	50.0	102	2	S29532	hypothetical prote
747	3	50.0	96	2	F69516	hypothetical prote	820	3	50.0	102	2	H64140	probable holo tr
748	3	50.0	97	2	S12958	tachykinin delta p	821	3	50.0	102	2	T46506	conserved hypothet
749	3	50.0	97	2	S26908	Ig heavy chain V r	822	3	50.0	101	2	AI0631	probable pheromone
750	3	50.0	97	2	PL0118	Ig heavy chain V-I	823	3	50.0	101	2	A71135	hypothetical prote
751	3	50.0	97	2	S26805	Ig heavy chain V r	824	3	50.0	102	2	T36592	hypothetical prote
752	3	50.0	97	2	S26804	Ig heavy chain V r	825	3	50.0	102	2	C72659	hypothetical prote
753	3	50.0	97	2	S14474	Ig heavy chain V r	826	3	50.0	102	2	T36592	hypothetical prote
754	3	50.0	97	2	S26806	Ig heavy chain V r	827	3	50.0	102	2	T36592	hypothetical prote
755	3	50.0	97	2	PH0876	Ig heavy chain V-I	828	3	50.0	102	2	S67179	probable membrane
756	3	50.0	97	2	G34964	Ig gamma chain V r	829	3	50.0	103	1	SKADC2	hexon-associated p
757	3	50.0	97	2	JH0428	Ig heavy chain V r	830	3	50.0	103	2	AI1275	thioredoxin homolo
758	3	50.0	97	2	S26898	Ig heavy chain V r	831	3	50.0	103	2	AI1275	thioredoxin homolo
759	3	50.0	97	2	S26906	Ig heavy chain V r	832	3	50.0	103	2	AI1638	thioredoxin homolo

833	3	50.0	103	2	B26167	Ig lambda chain C	906	109	2	E70956	hypothetical prote
834	3	50.0	103	2	C71085	hypothetical prote	907	109	2	G75484	hypothetical prote
835	3	50.0	103	2	A82121	conserved hypotet	908	109	2	F83457	hypothetical prote
836	3	50.0	103	2	A87435	hypothetical iIk p	909	109	2	F88021	protein w109.5 [i
837	3	50.0	103	2	JQ0700	hypothetical prote	910	109	2	PN0640	polyketide cyclase
838	3	50.0	103	2	S72917	hypothetical prote	911	109	2	C72588	hypothetical prote
839	3	50.0	103	2	D72710	hypothetical prote	912	110	1	RGSAMI	probable regulator
840	3	50.0	103	2	D71047	hypothetical prote	913	110	2	S24250	Ig heavy chain V r
841	3	50.0	104	2	T10287	hypothetical prote	914	110	2	A42573	exonuclease ABC c
842	3	50.0	104	2	S38104	hypothetical prote	915	110	2	S19454	exchangeable membrane
843	3	50.0	104	2	B81045	hypothetical prote	916	110	2	F72487	hypothetical prote
844	3	50.0	104	2	A72598	hypothetical prote	917	110	2	H72567	hypothetical prote
845	3	50.0	104	2	A82395	conserved hypotet	918	110	2	F91284	hypothetical prote
846	3	50.0	104	2	E87446	hypothetical prote	919	110	2	T12499	hypothetical prote
847	3	50.0	104	2	S17202	protein kinase (EC	920	110	2	T00142	hypothetical prote
848	3	50.0	104	2	F85359	hypothetical prote	921	110	2	AG2575	hypothetical prote
849	3	50.0	104	2	H70823	hypothetical prote	922	111	1	CCEI	cytochrome c - gre
850	3	50.0	104	2	D72744	hypothetical prote	923	111	2	AD2337	cytochrome c6 prec
851	3	50.0	104	2	AC0245	conserved hypotet	924	111	2	AD2337	cytochrome c6 (imp
852	3	50.0	105	1	TXFK	thioredoxin - cory	925	111	2	I39601	vpx protein - huma
853	3	50.0	105	2	H69517	thioredoxin (trx-4	926	111	2	S08438	conserved hypotet
854	3	50.0	105	2	AG2042	thioredoxin (impor	927	111	2	C83320	12K protein - phag
855	3	50.0	105	2	S44125	Ig lambda chain V	928	111	2	S56131	hypothetical prote
856	3	50.0	105	2	E82047	met repressor VC26	929	111	2	S64145	hypothetical prote
857	3	50.0	105	2	S41856	TyA protein - yeas	930	111	2	T37114	hypothetical prote
858	3	50.0	105	2	F85583	probable tail comp	931	111	2	T49549	hypothetical prote
859	3	50.0	105	2	AE0581	conserved hypotet	932	111	2	F82525	hypothetical prote
860	3	50.0	105	2	AE1046	SugE protein (impo	933	111	2	B84058	hypothetical prote
861	3	50.0	105	2	S11410	hypothetical prote	934	111	2	I38218	protein-serine/thr
862	3	50.0	105	2	F70587	hypothetical prote	935	111	2	F96590	hypothetical prote
863	3	50.0	105	2	E90831	probable holin pro	936	111	2	C71227	hypothetical prote
864	3	50.0	105	2	F90335	hypothetical prote	937	112	1	AI0587	hypothetical prote
865	3	50.0	105	2	AH3505	thioredoxin, proba	938	112	2	SPRFA	substance P alpha
866	3	50.0	105	2	C95223	thioredoxin, proba	939	112	2	T05118	leucoanthochryandin
867	3	50.0	105	2	G87591	hypothetical prote	940	112	2	B47033	AadA2 - Pseudomona
868	3	50.0	105	2	A83510	hypothetical prote	941	112	2	S12155	vpx protein - huma
869	3	50.0	105	2	A82456	probable acetyltra	942	112	2	G70855	hypothetical prote
870	3	50.0	105	2	S22603	hypothetical prote	943	112	2	S75152	hypothetical prote
871	3	50.0	106	2	E98087	conserved hypotet	944	112	2	T36564	probable SdhC subu
872	3	50.0	106	2	C69772	thioredoxin homolo	945	112	2	C72605	probable regulator
873	3	50.0	106	2	A82870	thioredoxin UUS89	946	112	2	H96031	probable transcrip
874	3	50.0	106	2	E84056	thioredoxin-H1 BH3	947	113	2	A34792	Ig heavy chain pre
875	3	50.0	106	2	S37454	Ig mu chain - huma	948	113	2	JI0049	Ig heavy chain V r
876	3	50.0	106	2	H71242	hypothetical prote	949	113	2	D71205	hypothetical prote
877	3	50.0	106	2	T36973	hypothetical prote	950	113	2	T44042	chemokine (impor
878	3	50.0	106	2	C87243	hypothetical prote	951	113	2	G81415	probable periplasm
879	3	50.0	106	2	G97594	hypothetical prote	952	113	2	C75263	hypothetical prote
880	3	50.0	106	2	C83584	conserved hypotet	953	113	2	A83444	probable lipase PA
881	3	50.0	106	2	A72581	hypothetical prote	954	113	2	AH0397	probable lipoprote
882	3	50.0	107	1	A26622	thioredoxin - Chro	955	114	1	GARB21	Ig heavy chain V-A
883	3	50.0	107	2	G69998	thioredoxin H1 hom	956	114	2	I50553	gonadotropin I bet
884	3	50.0	107	2	AH3504	thioredoxin C-1 [i	957	114	2	B34792	Ig heavy chain pre
885	3	50.0	107	2	B46516	Ig lambda chain V	958	114	2	I72667	cold agglutinin FS
886	3	50.0	107	2	C81172	hypothetical prote	959	114	2	S41365	genome polyprotein
887	3	50.0	107	2	B81935	hypothetical prote	960	114	2	S41359	genome polyprotein
888	3	50.0	107	2	F64037	hypothetical prote	961	114	2	S41362	genome polyprotein
889	3	50.0	107	2	E90976	hypothetical prote	962	114	2	S41358	genome polyprotein
890	3	50.0	107	2	C85823	hypothetical prote	963	114	2	S41366	genome polyprotein
891	3	50.0	107	2	AF0831	conserved hypotet	964	114	2	E71034	hypothetical prote
892	3	50.0	108	2	S21759	biphenyl dioxygena	965	114	2	T37926	hypothetical prote
893	3	50.0	108	2	S44190	genome polyprotein	966	114	2	D70469	hypothetical prote
894	3	50.0	108	2	AH0679	probable membrane	967	114	2	G69400	conserved hypotet
895	3	50.0	108	2	AH0176	probable sulfite r	968	114	2	G72510	hypothetical prote
896	3	50.0	108	2	S12193	hypothetical prote	969	114	2	H86625	hypothetical prote
897	3	50.0	108	2	G69261	hypothetical prote	970	114	2	Q00149	hypothetical 12.6K
898	3	50.0	108	2	F82598	hypothetical prote	971	114	2	G71161	hypothetical prote
899	3	50.0	108	2	G87087	probable membrane	972	115	1	SPREG	substance P gamma
900	3	50.0	108	2	C95312	hypothetical prote	973	115	2	T07783	leucoanthochryandin
901	3	50.0	109	1	D42409	biphenyl dioxygena	974	115	2	S47039	tachykinin I precu
902	3	50.0	109	1	E41858	biphenyl dioxygena	975	115	2	D34792	Ig heavy chain pre
903	3	50.0	109	1	JC4995	biphenyl dioxygena	976	115	2	C34792	Ig heavy chain pre
904	3	50.0	109	2	D50733	probable minor tai	977	115	2	S41364	genome polyprotein
905	3	50.0	109	2	B72615	hypothetical prote	978	115	2	AE3313	protein secretion

979	3	50.0	115	2	T17301	hypothetical prote
980	3	50.0	115	2	H75543	hypothetical prote
981	3	50.0	115	2	F72570	hypothetical prote
982	3	50.0	115	2	G72642	probable surface p
983	3	50.0	115	2	S04677	hypothetical prote
984	3	50.0	115	2	D71194	hypothetical prote
985	3	50.0	116	1	GARB15	Ig heavy chain V-A
986	3	50.0	116	2	F30517	Ig heavy chain pre
987	3	50.0	116	2	S37456	Ig mu chain - huma
988	3	50.0	116	2	B26340	Ig heavy chain pr
989	3	50.0	116	2	S18557	Ig heavy chain v r
990	3	50.0	116	2	A72263	response regulator
991	3	50.0	116	2	G54126	N-acetylmutamoyl-L
992	3	50.0	116	2	A95862	hypothetical prote
993	3	50.0	116	2	D95995	hypothetical prote
994	3	50.0	116	2	AC3319	integrase/recombin
995	3	50.0	116	2	T03472	conserved hypothet
996	3	50.0	116	2	D75355	hypothetical prote
997	3	50.0	116	2	T36999	probable transposa
998	3	50.0	116	2	B92270	hypothetical prote
999	3	50.0	117	1	HVMS8A	Ig heavy chain pre
1000	3	50.0	117	1	HVMS73	Ig heavy chain pre

ALIGNMENTS

RESULT 1

B83241
conserved hypothetical protein PA3230 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: B83241
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: B83241
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <STO>
A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06618.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA3230

Query Match

Best Local Similarity

Matches

5; Conservative

83.3%; Score 5; DB 2; Length 374;

100.0%; Pred. No. 19;

0; Mismatches

0; Indels

0; Gaps

0;

QY

2

DWSWA

6

|||||

Db

81

DWSWA

85

RESULT 2

E87304
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-889 <STO>

Query Match

Best Local Similarity

Matches

4; Conservative

66.7%; Score 4; DB 2; Length 37;

100.0%; Pred. No. 50;

0; Mismatches

0; Indels

0; Gaps

0;

QY

1

ADWS

4

|||||

Db

10

ADWS

13

A;Cross-references: GB:AE005673; NID:gl3421615; PIDN:AAK22433.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0446

Query Match

Best Local Similarity

Matches

5; Conservative

83.3%; Score 5; DB 2; Length 889;

100.0%; Pred. No. 40;

0; Mismatches

0; Indels

0; Gaps

0;

QY

1

ADMSW

5

|||||

Db

618

ADMSW

622

RESULT 3

A24047
gap junction protein, cardiac - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Jul-1999
C;Accession: A24047
R;Nicholson, B.J.; Gros, D.B.; Kent, S.B.H.; Hood, L.E.; Revel, J.P.
J. Biol. Chem. 260, 6514-6517, 1985
A;Title: The Mr 28,000 gap junction proteins from rat heart and liver are different but
A;Reference number: A92530; MUID:85207650; PMID:2987225
A;Accession: A24047
A;Molecule type: protein
A;Residues: 1-32 <NIC>
C;Superfamily: gap junction protein
C;Keywords: cardiac muscle; heart; transmembrane protein

Query Match

Best Local Similarity

Matches

4; Conservative

66.7%; Score 4; DB 2; Length 32;

100.0%; Pred. No. 44;

0; Mismatches

0; Indels

0; Gaps

0;

QY

1

ADWS

4

|||||

Db

1

ADWS

4

RESULT 4

A59401
delta-palut1 - Paracaelotes luctuosus
C;Species: Paracaelotes luctuosus
C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 17-May-2002
C;Accession: A59401
R;Corzo, G.
Eur. J. Biochem. 267, 5783-5795, 2000
A;Title: Isolation, synthesis and pharmacological characterization of delta-palutoxins I
A;Reference number: A59401
A;Accession: A59401
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-37 <COR>
A;Note: insect-specific sodium channel neurotoxin
C;Superfamily: curatatoxin
E;2-18/Disulfide bonds: #status experimental
E;9-23/Disulfide bonds: #status experimental
F;17-33/Disulfide bonds: #status experimental
F;25-31/Disulfide bonds: #status experimental

Query Match

Best Local Similarity

Matches

4; Conservative

66.7%; Score 4; DB 2; Length 37;

100.0%; Pred. No. 50;

0; Mismatches

0; Indels

0; Gaps

0;

QY

1

ADWS

4

|||||

Db

10

ADWS

13

RESULT 5

AG2302
hypothetical protein asl3974 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

Query Match

Best Local Similarity

Matches

4; Conservative

66.7%; Score 4; DB 2; Length 37;

100.0%; Pred. No. 50;

0; Mismatches

0; Indels

0; Gaps

0;

QY

1

ADWS

4

|||||

Db

10

ADWS

13

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG2302
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anaerostipes*
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AG2302
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <KUR>
A;Cross-references: GB:BA000019; PIDN:BA075673.1; PID:gl7133108; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: asl3974

Query Match 66.7%; Score 4; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 41 ADWS 44

RESULT 6
H95051
hypothetical protein SP0448 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C;Accession: H95051
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 458-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95051
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <KUR>
A;Cross-references: GB:AB005672; PIDN:AAK74609.1; PID:gl4971918; GSPDB:GN00164; TIGR:SP4
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0448

Query Match 66.7%; Score 4; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 18 ADWS 21

RESULT 7
D97922
hypothetical protein spr0404 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
C;Accession: D97922
R;Hoskins, J.A.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D97922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <KUR>

A;Cross-references: GB:AE007317; PIDN:AAK99208.1; PID:gl5457967; GSPDB:GN00174
C;Genetics:
A;Gene: spr0404

Query Match 66.7%; Score 4; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 18 ADWS 21

RESULT 8
T10250
lectin homolog 2 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10250
R;Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.
Plant Cell Physiol. 36, 1349-1359, 1995
A;Title: Cytokinin induces a rapid decrease in the levels of mRNAs for catalase, 3-hydroxy
A;Reference number: Z16946; MUID:96104306; PMID:8564304
A;Accession: T10250
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-94 <TOY>
A;Cross-references: EMBL:D63388; NID:gl199482; PIDN:BAA09704.1; PID:gl1199483
A;Experimental source: seedling; cotyledon

Query Match 66.7%; Score 4; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 35 WSWA 38

RESULT 9
T36897
probable xylanase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
C;Accession: T36897
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Accession: T36897
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-95 <SBE>
A;Cross-references: EMBL:AL096743; PIDN:CAB46384.1; GSPDB:GN00070; SCORDB:SCI7.01c
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCORDB:SCI7.01c
C;Superfamily: Xylan 1,4-beta-xylosidase (EC 3.2.1.37)

Query Match 66.7%; Score 4; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 18 ADWS 21

RESULT 10
E53374
type IV prepilin peptidase (EC 3.4.99.-) piliD - Neisseria subflava (strain LNP3260) (frag
N;Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
C;Species: Neisseria subflava
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 29-Jan-1999

C;Accession: E53374
R;Dupuy, B.; Pugsley, A.P.
J. Bacteriol. 176, 1323-1331, 1994
A;Title: Type IV prepilin peptidase gene of *Neisseria gonorrhoeae* MS11: presence of a re
A;Reference number: A53374; MUID:94156836; PMID:7906688
A;Accession: E53374
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-97 <DUP>
C;Genetics:
A;Gene: pilB
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine

Query Match 66.7%; Score 4; DB 2; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
DB 19 WSWA 22

RESULT 11
D53374
type IV prepilin peptidase (EC 3.4.99.-) - *Neisseria sicca* (strain LNP3265) (fragment)
N;Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
C;Species: *Neisseria sicca*
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 29-Jan-1999
C;Accession: D53374
R;Dupuy, B.; Pugsley, A.P.
J. Bacteriol. 176, 1323-1331, 1994
A;Title: Type IV prepilin peptidase gene of *Neisseria gonorrhoeae* MS11: presence of a re
A;Reference number: A53374; MUID:94156836; PMID:7906688
A;Accession: D53374
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-98 <DUP>
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine

Query Match 66.7%; Score 4; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WSWA 6
DB 20 WSWA 23

RESULT 12
H81042
hypothetical protein NMB1782 [imported] - *Neisseria meningitidis* (strain MC58 serogroup
C;Species: *Neisseria meningitidis*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: H81042; G81988
R;Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <TET>
A;Cross-references: GB:AE002528; GB:AE002098; NID:g7227034; PIDN:AAF42122.1; PID:g722703
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nucleur 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: G81988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-100 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CAB83970.1; PID:g737941
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1782; NMA0683; NMA0684
C;Superfamily: *Neisseria meningitidis* hypothetical protein NMB1782

Query Match 66.7%; Score 4; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSW 5
DB 77 DMSW 80

RESULT 13
T31781
hypothetical protein F13H6.2 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T31781
R;Jones, K.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A;Description: The sequence of *C. elegans* cosmid F13H6.
A;Reference number: Z21085
A;Accession: T31781
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-115 <JON>
A;Cross-references: EMBL:AF016437; PIDN:AA865884.1; GSPDB:GNO0023; CESP:F13H6.2
A;Experimental source: strain Bristol N2; clone F13H6
C;Genetics:
A;Gene: CESP:F13H6.2
A;Map position: 5
C;Introns: 52/1; 92/3
C;Superfamily: *Caenorhabditis elegans* hypothetical protein F13H6.2

Query Match 66.7%; Score 4; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 95 ADWS 98

RESULT 14
E90828
Probable terminase small subunit [imported] - *Escherichia coli* (strain O157:H7, substrain
C;Species: *Escherichia coli*
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: E90828
R;Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and gener
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90828
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <HAY>
A;Cross-references: GB:BA000007; PIDN:BA835020.1; PID:g13361061; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECs1597

Query Match 66.7%; Score 4; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||||

Db 35 ADWS 38

RESULT 15

B85686
unknown protein encoded by prophage CP-933C [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B85686
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, M.; Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: B85686
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <STO>
A:Cross-references: GB:AE005174; NID:g12514775; PIDN:AA855950.1; GSPDB:GN00145; UWGP:Z18
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z1853

Query Match 66.7%; Score 4; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||||

Db 35 ADWS 38

RESULT 16

S69909
Ig V-D-J region (MS) - human
C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C:Accession: S69909
R:Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A:Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multiple myeloma
A:Reference number: S69909; MUID:94335315; PMID:8057663
A:Accession: S69909
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-122 <SAH>
A:Cross-references: EMBL:Z33399; NID:9871348; PIDN:CAAB3850.1; PID:g871349
A:Note: the sequence of residues 112-122 and the corresponding nucleic acid sequence are identical
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:15-97/Domain: immunoglobulin homology <IMW>

Query Match 66.7%; Score 4; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
|||||

Db 33 DWSW 36

RESULT 17

E69973
hypothetical protein yrdN - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: E69973
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, A.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch, C.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: E69973
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-129 <KUN>
A:Molecule type: DNA
A:Cross-references: GB:Z99117; GB:AL009126; NID:g2634966; PIDN:CAB14607.1; PID:g2635111
A:Experimental source: strain 168
C:Genetics:
A:Gene: yrdN
C:Superfamily: hypothetical protein yrdN

Query Match 66.7%; Score 4; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||||

Db 113 ADWS 116

RESULT 18

F69902
conserved hypothetical protein yodA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: F69902
R:Kunst, F.; Ogawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter, C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch, C.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert, Iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: F69902
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-129 <KUN>
A:Molecule type: DNA
A:Cross-references: GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13844.1; PID:g2634345
A:Experimental source: strain 168
C:Genetics:
A:Gene: yodA
C:Superfamily: hypothetical protein yrdN

Query Match 66.7%; Score 4; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
|||||

Db 113 ADWS 116

```
RESULT 19
S65785
mel-13a protein - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 26-Aug-1999
C:Accession: S65785
R:Tetsu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.
Biochim. Biophys. Acta 1305, 109-112, 1996
A:Title: Cloning and characterization of two transcripts generated from the mel-13 gene
A:Reference number: S65785; MUID:96180310; PMID:8597592
A:Accession: S65785
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <TET>
A:Cross-references: EMBL:U35309
C:Genetics:
A:Gene: mel-13
C:Superfamily: mouse mel-13a protein
C:Keywords: alternative splicing

Query Match      66.7%; Score 4; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSW 5
Db      58 DWSW 61

RESULT 20
S70967
bfpG protein - Escherichia coli
C:Species: Escherichia coli
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Jun-2000
C:Accession: S70967
R:Stone, K.D.; Zhang, H.Z.; Carlson, L.K.; Donnenberg, M.S.
Mol. Microbiol. 20, 325-337, 1996
A:Title: A cluster of fourteen genes from enteropathogenic Escherichia coli is sufficient
A:Reference number: S70966; MUID:96310370; PMID:8733231
A:Accession: S70967
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-133 <STO>
A:Cross-references: EMBL:Z68186; NID:gl122399; PIDN:CAA92327.1; PID:gl122401
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C:Genetics:
A:Gene: bfpG
A:Start codon: GTG
C:Superfamily: Escherichia coli bfpG protein

Query Match      66.7%; Score 4; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      50 ADWS 53

RESULT 21
F84190
hypothetical protein Vng0311h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: F84190
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leitchauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: F84190
```

```
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <STO>
A:Cross-references: GB:AE004437; NID:gl0579938; PIDN:AAG18890.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0311H
```

```
Query Match      66.7%; Score 4; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWS 4
Db      78 ADWS 81
```

```
RESULT 22
AG2926
conserved hypothetical protein Atu3013 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AG2926
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.;
erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG2926
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL43829.1; PID:gl7741370; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3013
A:Map position: linear chromosome
```

```
Query Match      66.7%; Score 4; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 ADWS 4
Db      20 ADWS 23
```

```
RESULT 23
H98355
hypothetical protein AGR_L_3577 [imported] - Agrobacterium tumefaciens (strain C58, Cerc
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: H98355
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: H98355
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-134 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK90370.1; PID:gl5160412; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_3577
A:Map position: linear chromosome
```

```
Query Match      66.7%; Score 4; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```


Qy 1 ADWS 4
Db 20 ADWS 23

RESULT 24
B83440
hypothetical protein PA1645 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83440
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:2043737; PMID:10984043
A:Accession: B83440
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-135 <STO>
A:Cross-references: GB:AB004592; GB:AB004091; NID:g9947609; PIDN:AG05034.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1645

Query Match 66.7%; Score 4; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 19 ADWS 22

RESULT 25
G84174
hypothetical protein Vng0143h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: G84174
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: G84174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-137 <STO>
A:Cross-references: GB:AB004437; NID:g10579791; PIDN:AAG18763.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0143H

Query Match 66.7%; Score 4; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 92 ADWS 95

RESULT 26
S54229
Ig mu heavy chain V region precursor - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S54229
R:Dufour, V.; Nau, F.
submitted to the EMBL Data Library, April 1995

A:Description: Sheep immunoglobulin mu heavy chain variable region sequence.
A:Reference number: S54225
A:Accession: S54229
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <DUF>
A:Cross-references: EMBL:Z49163; NID:g794097; PIDN:CAA89032.1; PID:g794098
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 4; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 118 WSWA 121

RESULT 27
A33155
pathogenesis-related protein 1 - maize
C:Species: Zea mays (maize)
C>Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 31-Dec-1993
C:Accession: A33155
R:Gillikin, J.; Burkhardt, W.; Graham, J.S.
submitted to the Protein Sequence Database, February 1991
A:Reference number: A33155
A:Accession: A33155
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-140 <GIL>
C:Superfamily: pathogenesis-related leaf protein

Query Match 66.7%; Score 4; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 64 ADWS 67

RESULT 28
T16896
hypothetical protein T19D7.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C:Accession: T16896
R:Minx, P.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid T19D7.
A:Reference number: Z18600
A:Accession: T16896
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-143 <MIN>
A:Cross-references: EMBL:U56961; NID:g1293805; PID:g1293807; PIDN:AAA98712.1; GSPDB:GN00
A:Experimental source: strain Bristol N2; clone T19D7
C:Genetics:
A:Gene: CESP:T19D7.2
A:Map position: X
A:Introns: 28/3; 52/1; 113/2
C:Superfamily: Caenorhabditis elegans hypothetical protein T19D7.2

Query Match 66.7%; Score 4; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 120 ADWS 123

```

A;Residues: 1-151 <PAR>
A;Cross-references: GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84906.1; PID:g738031;
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1678

Query Match      66.7%; Score 4; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      39 ADWS 42

RESULT 32
AI3271
acetyltransferase (EC 2.3.1.1-) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AI3271
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.;
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letescq;
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis;
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-152 <KUR>
A;Cross-references: GB:AE008917; PIDN:AAL51340.1; PID:g17982038; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0158
A;Map position: I
C;Keywords: acyltransferase

Query Match      66.7%; Score 4; DB 2; Length 152;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      141 ADWS 144

RESULT 33
B71131
hypothetical protein PH0815 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71131
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine;
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic al;
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71131
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-153 <KAW>
A;Cross-references: GB:AP000003; NID:g3236130; PIDN:BAA29908.1; PID:g3257225
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank;
C;Genetics:
A;Gene: PH0815
C;Superfamily: Pyrococcus horikoshii hypothetical protein PH0815

Query Match      66.7%; Score 4; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSW 5

gene 29 protein - Mycobacterium phase L5
S30974
C;Species: Mycobacterium phase L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Nov-1999
C;Accession: S30974
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans;
A;Reference number: S30949; MUID:93211283; PMID:8459767
A;Accession: S30974
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-147 <DON>
A;Cross-references: EMBL:Z18946; NID:gl5859; PIDN:CMA79405.1; PID:gl5885
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
A;Gene: 29
C;Superfamily: Mycobacterium phase L5 gene 29 protein

Query Match      66.7%; Score 4; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      40 ADWS 43

RESULT 30
C72803
gp29 protein - Mycobacterium phase D29
C;Species: Mycobacterium phase D29
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 20-Apr-2001
C;Accession: C72803
R;Ford, M.E.; Sarkis, G.J.; Belanger, A.E.; Hendrix, R.W.; Hatfull, G.F.
J. Mol. Biol. 279, 143-164, 1998
A;Title: Genome structure of mycobacteriophage D29: Implications for phage evolution.
A;Reference number: A72800; MUID:98300335; PMID:9636706
A;Accession: C72803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <FOR>
A;Cross-references: GB:AF022214; NID:g3172250; PIDN:AAC18470.1; PID:g3172277
C;Genetics:
A;Gene: 29
C;Superfamily: Mycobacterium phase L5 gene 29 protein

Query Match      66.7%; Score 4; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      40 ADWS 43

RESULT 31
A81863
hypothetical protein NMA1678 [imported] - Neisseria meningitidis (strain Z2491 serogroup;
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81863
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel;
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81863
A;Status: preliminary
A;Molecule type: DNA
```

Db 125 DWSW 128
|||||
RESULT 34
A97671
C:Species: Agrobacterium tumefaciens (strain C58, Cerc
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: A97671
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:21608551; PMID:11743194
A:Accession: A97671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-161 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK88322.1; PID:gl5157798; GSPDB:GN00169
C:Genetics:
A:Gene: AGR C.4708
A:Map position: circular chromosome
Query Match 66.7%; Score 4; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWS 4
|||||
Db 34 ADWS 37
RESULT 35
T02054
C:Species: Zea mays (maize)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 11-May-2000
C:Accession: T02054
R:Morris, S.W.; Vernooij, B.; Titatarn, S.; Starrett, M.; Thomas, S.; Wiltse, C.C.; Fred
Mol. Plant Microbe Interact. 11, 643-658, 1998
A:Title: Induced resistance responses in maize.
A:Reference number: 214524; PMID:98313983; PMID:9650297
A:Accession: T02054
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-163 <MOR>
A:Cross-references: EMBL:U82200; NID:g3290003; PIDN:AAC25629.1; PID:g3290004
C:Genetics:
A:Gene: PR-1
C:Superfamily: pathogenesis-related leaf protein
Query Match 66.7%; Score 4; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWS 4
|||||
Db 87 ADWS 90
RESULT 36
AE0773
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AE0773
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A:Reference number: AB0502; PMID:21534947; PMID:11677608
A:Accession: AE0773
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-166 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02507.1; PID:gl6503371; GSPDB:GN00176
C:Genetics:
A:Gene: STY2358
Query Match 66.7%; Score 4; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 WSWA 6
|||||
Db 133 WSWA 136
RESULT 37
A35209
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 11-Jun-1999
C:Accession: A35209; S12724; S04070; S04593; S14190; S65373
R:Yamada, M.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biol. Chem. 265, 7687-7692, 1990
A:Title: Structural organization of the rat cytochrome c oxidase subunit IV gene.
A:Reference number: A35209; PMID:90237079; PMID:2159010
A:Accession: A35209
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <YAM>
A:Cross-references: GB:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R:Amuro, N.; Yamada, M.; Goto, Y.; Okazaki, T.
Nucleic Acids Res. 18, 3992, 1990
A:Title: Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase subunit
A:Reference number: S12724; PMID:90326528; PMID:2165254
A:Accession: S12724
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-169 <AMU>
A:Cross-references: EMBL:J05425; NID:g203516; PIDN:AAA40949.1; PID:g203517
R:Goto, Y.; Amuro, N.; Okazaki, T.
Nucleic Acids Res. 17, 2851, 1989
A:Title: Nucleotide sequence of cDNA for rat brain and liver cytochrome c oxidase subunit
A:Reference number: S04070; PMID:89240039; PMID:2541414
A:Accession: S04070
A:Molecule type: mRNA
A:Residues: 1-169 <GOT>
A:Cross-references: EMBL:X14209; NID:g55989; PIDN:CAA32426.1; PID:g55990
R:Gopalan, G.; Droste, M.; Kadenbach, B.
Nucleic Acids Res. 17, 4376, 1989
A:Title: Nucleotide sequence of cDNA encoding subunit IV of cytochrome c oxidase from fat
A:Reference number: S04593; PMID:89296488; PMID:2544859
A:Accession: S04593
A:Molecule type: mRNA
A:Residues: 1-169 <GOP>
A:Cross-references: EMBL:X15029; NID:g55980; PIDN:CAA33133.1; PID:g55981
R:Virbasius, J.V.; Scarpulla, R.C.
Nucleic Acids Res. 18, 6581-6586, 1990
A:Title: The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hormonal
A:Reference number: S14190; PMID:91067442; PMID:2174541
A:Accession: S14190
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-169 <VIR>
A:Cross-references: EMBL:X54081; NID:g57030; PIDN:CAA38018.1; PID:g57031
A:Experimental source: strain Sprague Dawley
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65373
A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-45 <SCH>
C;Genetics:
A;Gene: RCO4-1
A;Introns: 25/1; 81/1; 125/1
C;Function:
A;Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecules from the mitochondrial matrix producing two molecules of water and lowering the concentration of cytochrome-c oxidase chain IV
A;Pathway: oxidative phosphorylation; respiratory chain
C;Superfamily: cytochrome-c oxidase chain IV
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
F;1-22/Domain: transit peptide (mitochondrion) #status predicted <TRN>
F;23-169/Product: cytochrome-c oxidase chain IV #status experimental <MAT>
F;77-103/Domain: transmembrane helix #status predicted <TR01>

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 68 ADWS 71

RESULT 38
S12142
cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S12142; S16114
R;Grossman, L.I.; Akamatsu, M.
Nucleic Acids Res. 18, 6454, 1990
A;Title: Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c oxidase.
A;Reference number: S12142; MUID:91057158; PMID:2173832
A;Accession: S12142
A;Molecule type: mRNA
A;Residues: 1-169 <GRO>
A;Cross-references: EMBL:X54591; NID:g50518; PIDN:CAA38507.1; PID:g50519
A;Experimental source: strain Balb/c
R;Carter, R.S.; Avadhani, N.G.
Arch. Biochem. Biophys. 288, 97-106, 1991
A;Title: Cloning and characterization of the mouse cytochrome c oxidase subunit IV gene.
A;Reference number: S16114; MUID:91378465; PMID:1654830
A;Accession: S16114
A;Molecule type: mRNA
A;Residues: 1-169 <ARC>
C;Genetics:
A;Gene: COXIV
A;Genome: nuclear
C;Superfamily: cytochrome-c oxidase chain IV
C;Keywords: membrane-associated complex; mitochondrion; oxidative phosphorylation; oxidoreductase
F;1-22/Domain: transit peptide (mitochondrion) #status predicted <TRN>
F;23-169/Product: cytochrome-c oxidase chain IV #status predicted <MAT>

Query Match 66.7%; Score 4; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 68 ADWS 71

RESULT 39
F82952
ATP synthase delta chain PA5557 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 03-Jun-2002
C;Accession: F82952
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F82952
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-178 <STO>
A;Cross-references: GB:AE004967; GB:AE004091; NID:g9951884; PIDN:AAG08942.1; GSPDB:GN001;
A;Experimental source: strain PA01
C;Genetics:
A;Gene: atpH; PA5557
C;Superfamily: H+-transporting ATP synthase delta chain

Query Match 66.7%; Score 4; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 26 ADWS 29

RESULT 40
H83256
hypothetical protein PA3109 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 24-Aug-2001
C;Accession: H83256
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, S.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-180 <STO>
A;Cross-references: GB:AE004735; GB:AE004091; NID:g9949216; PIDN:AAG06497.1; GSPDB:GN001;
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3109
C;Superfamily: dedE protein

Query Match 66.7%; Score 4; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
DB 147 ADWS 150

RESULT 41
G84323
50S ribosomal protein L18P [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: G84323
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; La
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84323
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <STO>
A;Cross-references: GB:AE004437; NID:g10581178; PIDN:AAG19955.1; GSPDB:GN00138

C;Genetics:
A;Gene: rpl18p
C;Superfamily: rat ribosomal protein L5

Query Match 66.7%; Score 4; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 138 ADWS 141

RESULT 42
T28707
hypothetical protein T21D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 06-Oct-2000
C;Accession: T28707
R;Woessner, J.
submitted to the EMBL Data Library, August 1997
A;Description: The sequence of C. elegans cosmid T21D12.
A;Reference number: Z20514
A;Accession: T28707
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-185 <WOE>
A;Cross-references: EMBL:AF016687; PIDN:AAC48089.1; GSPDB:GN00022; CESP:T21D12.1
A;Experimental source: strain Bristol N2; clone T21D12
C;Genetics:
A;Gene: CESP:T21D12.1
A;Map position: 4
A;Introns: 17/1; 51/1; 127/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M02B7.2

Query Match 66.7%; Score 4; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 95 ADWS 98

RESULT 43
F95944
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: F95944
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95944
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <KUR>
A;Cross-references: GB:AL591985; PIDN:CAC49222.1; PID:gl5140708; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMD21156
A;Genome: plasmid

Query Match 66.7%; Score 4; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 59 ADWS 62

RESULT 44
AC0619
hypothetical bacteriophage protein STY1027 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0619
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05421.1; PID:gl6502182; GSPDB:GN00176
C;Genetics:
A;Gene: STY1027

Query Match 66.7%; Score 4; DB 2; Length 190;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 55 ADWS 58

RESULT 45
H69387
conserved hypothetical protein AF1105 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C;Accession: H69387
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uitterlinden, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: H69387
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <KLE>
A;Cross-references: GB:AE001027; GB:AE000782; NID:g2689350; PIDN:AAB90133.1; PID:g2649475

Query Match 66.7%; Score 4; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 98 ADWS 101

RESULT 46
G87453
RNA polymerase sigma-70 factor, ECF subfamily [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus

C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: G87453
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87453
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <STO>
A:Cross-references: GB:AE005673; NID:gl3423053; PIDN:AAK23627.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC1649

Query Match 66.7%; Score 4; DB 2; Length 194;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 148 ADWS 151

RESULT 47
G87510
hypothetical protein CC2112 [imported] - *Caulobacter crescentus*
C:Species: *Caulobacter crescentus*
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: G87510
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: G87510
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <STO>
A:Cross-references: GB:AE005673; NID:gl3423599; PIDN:AAK24083.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC2112

Query Match 66.7%; Score 4; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 160 WSWA 163

RESULT 48
E70423
conserved hypothetical protein aq_1421 - *Aquifex aeolicus*
C:Species: *Aquifex aeolicus*
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: E70423
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: E70423
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-197 <AQF>
A:Cross-references: GB:AE000739; NID:g2983813; PIDN:AAC07381.1; PID:g2983825; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: aq_1421

Query Match 66.7%; Score 4; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 51 WSWA 54

RESULT 49
G95219
HAM1 protein [imported] - *Streptococcus pneumoniae* (strain TIGR4)
C:Species: *Streptococcus pneumoniae*
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95219
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95219
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75952.1; PID:gl14973383; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI880

Query Match 66.7%; Score 4; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 135 ADWS 138

RESULT 50
T35699
probable sigma factor - *Streptomyces coelicolor*
C:Species: *Streptomyces coelicolor*
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 21-Jan-2000
C:Accession: T35699
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z21548
A:Accession: T35699
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-200 <MUR>
A:Cross-references: EMBL:AL021411; PIDN:CAA16191.1; GSPDB:GN00070; SCOEDB:SC7H1.04
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC7H1.04
C:Superfamily: transcription initiation factor sigma E

Query Match 66.7%; Score 4; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 38 ADWS 41

Search completed: July 23, 2004, 13:27:53
Job time : 30 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 13:27:25 ; Search time 42 Seconds
(without alignments)
44.736 Million cell updates/sec

Title: US-09-847-940C-6

Perfect score: 6

Sequence: 1 ADNSWA 6

Scoring table: OLIGO 60.0 , Gapext 60.0

Searched: 1288442 seqs, 313154207 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1288442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	10	US-09-847-946A-71
2	6	100.0	6	10	US-09-847-946A-73
3	6	100.0	7	10	US-09-847-946A-77
4	6	100.0	8	10	US-09-847-946A-70
5	6	100.0	8	10	US-09-847-946A-78
6	6	100.0	9	10	US-09-847-946A-69
7	6	100.0	9	10	US-09-847-946A-72
8	6	100.0	9	10	US-09-847-946A-75
9	6	100.0	9	10	US-09-847-946A-76
10	6	100.0	10	10	US-09-847-946A-71
11	6	100.0	10	10	US-09-847-946A-74
12	6	100.0	11	10	US-09-847-946A-68
13	5	83.3	6	9	US-09-847-940B-4
14	5	83.3	6	9	US-09-847-940B-5
15	5	83.3	6	10	US-09-847-946A-4
16	5	83.3	6	10	US-09-847-946A-5
17	5	83.3	6	10	US-09-847-946A-39
18	5	83.3	6	10	US-09-847-946A-40
19	5	83.3	6	10	US-09-847-946A-51
20	5	83.3	6	10	US-09-847-946A-62
21	5	83.3	7	10	US-09-847-946A-55
22	5	83.3	7	10	US-09-847-946A-66
23	5	83.3	8	10	US-09-847-946A-48
24	5	83.3	8	10	US-09-847-946A-56
25	5	83.3	8	10	US-09-847-946A-59
26	5	83.3	9	10	US-09-847-946A-67
27	5	83.3	9	10	US-09-847-946A-47
28	5	83.3	9	10	US-09-847-946A-50
29	5	83.3	9	10	US-09-847-946A-53
30	5	83.3	9	10	US-09-847-946A-54
31	5	83.3	9	10	US-09-847-946A-58
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35	5	83.3	10	10	US-09-847-946A-49
36	5	83.3	10	10	US-09-847-946A-52
37	5	83.3	10	10	US-09-847-946A-57
38	5	83.3	10	10	US-09-847-946A-60
39	5	83.3	10	10	US-09-847-946A-63
40	5	83.3	11	10	US-09-847-946A-46
41	5	83.3	14	12	US-10-424-593-199086
42	5	83.3	174	14	US-10-219-220-163
43	5	83.3	225	14	US-10-219-220-162
44	5	83.3	236	12	US-10-441-625-17
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46	5	83.3	277	14	US-10-219-220-280
47	5	83.3	312	14	US-10-306-762-23
48	5	83.3	378	14	US-10-219-220-158
49	5	83.3	501	14	US-10-171-311-234
50	5	83.3	605	14	US-10-156-761-9070
51	5	83.3	5435	16	US-10-203-295-38
52	4	66.7	6	9	US-09-847-940B-2
53	4	66.7	6	10	US-09-847-946A-33
54	4	66.7	7	10	US-09-847-946A-37
55	4	66.7	8	10	US-09-847-946A-30
56	4	66.7	8	10	US-09-847-946A-38
57	4	66.7	9	10	US-09-847-946A-29
58	4	66.7	9	10	US-09-847-946A-32
59	4	66.7	9	10	US-09-847-946A-35
60	4	66.7	9	10	US-09-847-946A-36
61	4	66.7	10	10	US-09-847-946A-31
62	4	66.7	10	10	US-09-847-946A-34
63	4	66.7	11	10	US-09-847-946A-28
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65	4	66.7	11	10	US-09-847-946A-140
66	4	66.7	12	10	US-09-847-946A-43
67	4	66.7	12	10	US-09-954-385-340
68	4	66.7	13	10	US-09-847-946A-143
69	4	66.7	13	10	US-09-847-946A-144
70	4	66.7	13	10	US-09-847-946A-145
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72	4	66.7	17	10	US-09-847-946A-141
73	4	66.7	17	10	US-09-847-946A-142
74	4	66.7	17	10	US-09-847-946A-146
75	4	66.7	17	10	US-09-847-946A-147
76	4	66.7	18	10	US-09-847-946A-131
77	4	66.7	18	10	US-09-847-946A-135
78	4	66.7	18	10	US-09-847-946A-136
79	4	66.7	21	12	US-10-609-217-866
80	4	66.7	21	12	US-10-632-388-866
81	4	66.7	21	12	US-10-651-723-866
82	4	66.7	21	12	US-10-645-761-866
83	4	66.7	21	16	US-10-666-696-866
84	4	66.7	21	16	US-10-653-048-866
85	4	66.7	22	10	US-09-847-946A-133
86	4	66.7	22	10	US-09-847-946A-134
87	4	66.7	22	10	US-09-847-946A-137
88	4	66.7	22	10	US-09-847-946A-138

89	4	66.7	22	10	US-09-847-946A-138	Sequence 138, App	162	4	66.7	99	10	US-09-764-891-3660	Sequence 3660, Ap
90	4	66.7	22	10	US-09-847-946A-139	Sequence 139, App	163	4	66.7	101	15	US-10-094-749-2322	Sequence 2322, Ap
91	4	66.7	22	12	US-09-974-131A-12	Sequence 12, Appl	164	4	66.7	105	15	US-10-108-260A-4429	Sequence 4429, Ap
92	4	66.7	22	14	US-10-120-604-57	Sequence 57, Appl	165	4	66.7	106	12	US-10-424-599-211159	Sequence 211159,
93	4	66.7	22	14	US-10-278-314-12	Sequence 12, Appl	166	4	66.7	106	12	US-10-424-599-282413	Sequence 282413,
94	4	66.7	25	9	US-09-864-761-46354	Sequence 46354, A	167	4	66.7	114	15	US-10-264-237-2077	Sequence 2077, Ap
95	4	66.7	26	9	US-09-814-452-21	Sequence 21, Appl	168	4	66.7	115	12	US-10-220-120-321	Sequence 321, App
96	4	66.7	28	9	US-09-847-940B-18	Sequence 18, Appl	169	4	66.7	116	12	US-10-424-599-192081	Sequence 192081,
97	4	66.7	28	10	US-09-847-946A-18	Sequence 18, Appl	170	4	66.7	117	10	US-09-809-391-360	Sequence 360, App
98	4	66.7	28	12	US-10-602-303-2	Sequence 2, Appli	171	4	66.7	117	10	US-09-882-171-360	Sequence 360, App
99	4	66.7	29	10	US-09-962-756-1410	Sequence 1410, Ap	172	4	66.7	117	12	US-10-424-599-228673	Sequence 228673,
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101	4	66.7	29	16	US-10-253-493-1410	Sequence 1410, Ap	174	4	66.7	117	15	US-10-108-260A-2639	Sequence 2639, Ap
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103	4	66.7	36	10	US-09-962-756-1320	Sequence 1320, Ap	176	4	66.7	119	15	US-10-104-047-3261	Sequence 3261, Ap
104	4	66.7	36	15	US-10-253-471-1320	Sequence 1320, Ap	177	4	66.7	119	16	US-10-389-566-475	Sequence 475, App
105	4	66.7	36	16	US-10-253-493-1320	Sequence 1320, Ap	178	4	66.7	120	16	US-10-437-963-118076	Sequence 118076,
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107	4	66.7	40	12	US-10-424-599-169200	Sequence 169200,	180	4	66.7	121	16	US-10-437-963-115821	Sequence 115821,
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110	4	66.7	51	16	US-10-109-048-1088	Sequence 1088, Ap	183	4	66.7	123	15	US-10-437-963-117147	Sequence 117147,
111	4	66.7	51	16	US-10-109-048-1093	Sequence 1093, Ap	184	4	66.7	125	12	US-10-424-599-143106	Sequence 143106,
112	4	66.7	52	16	US-10-109-048-1085	Sequence 1085, Ap	185	4	66.7	125	16	US-10-437-963-119236	Sequence 119236,
113	4	66.7	52	16	US-10-109-048-1086	Sequence 1086, Ap	186	4	66.7	126	15	US-10-108-260A-2502	Sequence 2502, Ap
114	4	66.7	52	16	US-10-109-048-1090	Sequence 1090, Ap	187	4	66.7	127	12	US-10-425-114-40528	Sequence 40528, A
115	4	66.7	52	16	US-10-109-048-1091	Sequence 1091, Ap	188	4	66.7	128	14	US-10-279-029-105	Sequence 105, App
116	4	66.7	52	16	US-10-109-048-1092	Sequence 1092, Ap	189	4	66.7	129	16	US-10-437-963-108791	Sequence 108791,
117	4	66.7	52	16	US-10-109-048-1094	Sequence 1094, Ap	190	4	66.7	129	16	US-10-437-963-137466	Sequence 137466,
118	4	66.7	55	9	US-09-814-452-13	Sequence 13, Appl	191	4	66.7	132	12	US-10-424-599-207797	Sequence 207797,
119	4	66.7	56	9	US-09-814-452-11	Sequence 11, Appl	192	4	66.7	133	12	US-10-424-599-207797	Sequence 207797,
120	4	66.7	57	16	US-10-437-963-116410	Sequence 116410,	193	4	66.7	135	11	US-09-864-408A-6096	Sequence 6096, Ap
121	4	66.7	61	9	US-09-796-692-1003	Sequence 1003, Ap	194	4	66.7	136	12	US-10-424-599-279912	Sequence 279912,
122	4	66.7	61	14	US-10-040-862-1003	Sequence 1003, Ap	195	4	66.7	136	12	US-10-424-599-284094	Sequence 284094,
123	4	66.7	61	15	US-10-057-475B-1003	Sequence 1003, Ap	196	4	66.7	140	9	US-09-764-864-1379	Sequence 1379, Ap
124	4	66.7	61	15	US-10-354-884B-1003	Sequence 1003, Ap	197	4	66.7	144	12	US-10-282-122A-46942	Sequence 46942, A
125	4	66.7	61	16	US-10-437-963-146948	Sequence 146948,	198	4	66.7	144	14	US-10-101-464A-739	Sequence 739, App
126	4	66.7	63	12	US-10-424-599-208480	Sequence 208480,	199	4	66.7	146	12	US-10-282-122A-46540	Sequence 46540, A
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128	4	66.7	64	12	US-10-424-599-273932	Sequence 273932,	201	4	66.7	149	12	US-10-424-599-157816	Sequence 157816,
129	4	66.7	66	12	US-10-424-599-207854	Sequence 207854,	202	4	66.7	149	12	US-10-424-599-263312	Sequence 263312,
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135	4	66.7	73	16	US-10-437-963-155224	Sequence 155224,	208	4	66.7	153	9	US-09-925-301-1367	Sequence 1367, Ap
136	4	66.7	74	12	US-10-424-599-149447	Sequence 149447,	209	4	66.7	153	12	US-10-425-114-39069	Sequence 39069, A
137	4	66.7	74	14	US-10-106-698-7099	Sequence 7099, Ap	210	4	66.7	150	12	US-10-282-122A-68173	Sequence 68173, A
138	4	66.7	75	16	US-10-109-048-1150	Sequence 1150, Ap	211	4	66.7	161	16	US-10-437-963-157766	Sequence 157766,
139	4	66.7	76	12	US-10-424-599-251348	Sequence 251348,	212	4	66.7	163	9	US-09-840-479-13	Sequence 13, Appl
140	4	66.7	78	9	US-09-071-838-184	Sequence 184, App	213	4	66.7	163	13	US-10-078-929-202	Sequence 202, App
141	4	66.7	78	12	US-10-425-114-42667	Sequence 42667, A	214	4	66.7	167	12	US-10-220-120-419	Sequence 419, App
142	4	66.7	78	14	US-10-213-512-184	Sequence 184, App	215	4	66.7	167	12	US-10-220-120-419	Sequence 419, App
143	4	66.7	78	16	US-10-437-963-189019	Sequence 189019,	216	4	66.7	168	15	US-10-094-749-1806	Sequence 1806, Ap
144	4	66.7	80	12	US-10-424-599-255598	Sequence 255598,	217	4	66.7	170	10	US-09-975-719-339	Sequence 339, App
145	4	66.7	82	11	US-09-833-245-1600	Sequence 1600, Ap	218	4	66.7	170	12	US-10-087-193-1047	Sequence 1047, Ap
146	4	66.7	82	12	US-10-424-599-263066	Sequence 263066,	219	4	66.7	173	12	US-10-437-963-194553	Sequence 194553,
147	4	66.7	82	16	US-10-437-963-137643	Sequence 137643,	220	4	66.7	174	16	US-10-282-122A-66851	Sequence 66851, A
148	4	66.7	84	12	US-10-425-114-37259	Sequence 37259, A	221	4	66.7	178	16	US-10-437-963-132349	Sequence 132349,
149	4	66.7	86	12	US-09-978-360A-584	Sequence 584, App	222	4	66.7	178	16	US-10-437-963-132349	Sequence 132349,
150	4	66.7	88	12	US-10-424-599-210535	Sequence 210535,	223	4	66.7	180	16	US-10-437-963-185888	Sequence 185888,
151	4	66.7	88	12	US-10-424-599-273840	Sequence 273840,	224	4	66.7	181	14	US-10-156-761-11638	Sequence 11638, A
152	4	66.7	90	12	US-10-424-599-249015	Sequence 249015,	225	4	66.7	182	14	US-10-425-114-57909	Sequence 57909, A
153	4	66.7	90	12	US-10-424-599-261138	Sequence 261138,	226	4	66.7	188	12	US-10-425-114-47742	Sequence 47742, A
154	4	66.7	92	14	US-10-029-386-29710	Sequence 29710, A	227	4	66.7	190	12	US-09-978-360A-488	Sequence 488, App
155	4	66.7	92	14	US-10-029-386-29710	Sequence 29710, A	228	4	66.7	190	12	US-09-978-360A-488	Sequence 488, App
156	4	66.7	94	9	US-09-864-761-41701	Sequence 41701, A	229	4	66.7	190	12	US-10-425-114-71389	Sequence 71389, A
157	4	66.7	94	12	US-10-424-599-261839	Sequence 261839,	230	4	66.7	195	15	US-10-094-749-3275	Sequence 3275, Ap
158	4	66.7	95	12	US-10-424-599-167617	Sequence 167617,	231	4	66.7	201	14	US-10-156-761-8837	Sequence 8837, Ap
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160	4	66.7	97	16	US-10-437-963-139350	Sequence 139350,	233	4	66.7	202	12	US-10-424-599-150612	Sequence 150612,
161	4	66.7	98	10	US-09-764-891-4516	Sequence 4516, Ap	234	4	66.7	202	15	US-10-104-047-2736	Sequence 2736, Ap
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236	4	66.7	207	12	US-10-424-599-170021	Sequence 170021, Ap	309	4	66.7	233	16	US-10-437-963-151143	Sequence 151143, Ap
237	4	66.7	210	15	US-10-264-049-3180	Sequence 3180, Ap	310	4	66.7	234	14	US-10-294-524-1	Sequence 1, Appli
238	4	66.7	212	14	US-10-319-799-69	Sequence 69, Appli	311	4	66.7	234	16	US-10-437-963-158062	Sequence 158062, A
239	4	66.7	213	9	US-09-756-998-4	Sequence 4, Appli	312	4	66.7	235	12	US-10-425-114-50984	Sequence 50984, A
240	4	66.7	213	14	US-10-156-761-11043	Sequence 11043, A	313	4	66.7	235	14	US-10-316-253-271	Sequence 271, App
241	4	66.7	215	12	US-10-425-114-37563	Sequence 37563, A	314	4	66.7	236	16	US-10-437-963-183286	Sequence 183286, A
242	4	66.7	215	12	US-10-425-114-62345	Sequence 62345, A	315	4	66.7	239	12	US-10-425-114-53040	Sequence 53040, A
243	4	66.7	217	16	US-10-437-963-142818	Sequence 142818, A	316	4	66.7	300	14	US-10-306-763-80	Sequence 80, Appli
244	4	66.7	220	14	US-10-211-160-8	Sequence 8, Appli	317	4	66.7	300	16	US-10-437-963-123340	Sequence 123340, A
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252	4	66.7	232	12	US-10-425-114-37131	Sequence 37131, A	325	4	66.7	306	14	US-10-166-984-2	Sequence 2, Appli
253	4	66.7	232	14	US-10-156-761-10287	Sequence 10287, A	326	4	66.7	306	15	US-10-166-984-2	Sequence 2, Appli
254	4	66.7	232	14	US-10-156-761-11822	Sequence 11822, A	327	4	66.7	308	12	US-10-147-493-100	Sequence 100, App
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257	4	66.7	237	12	US-10-282-122A-60688	Sequence 60688, A	330	4	66.7	308	12	US-10-143-118-100	Sequence 100, App
258	4	66.7	238	12	US-10-441-625-15	Sequence 15, Appli	331	4	66.7	308	12	US-10-144-993-100	Sequence 100, App
259	4	66.7	238	14	US-10-441-626-15	Sequence 15, Appli	332	4	66.7	308	12	US-10-158-787-100	Sequence 100, App
260	4	66.7	239	12	US-10-425-114-68853	Sequence 68853, A	333	4	66.7	308	12	US-10-140-024-100	Sequence 100, App
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262	4	66.7	239	14	US-10-441-626-7	Sequence 7, Appli	335	4	66.7	308	12	US-10-152-405-100	Sequence 100, App
263	4	66.7	243	12	US-10-425-114-70901	Sequence 70901, A	336	4	66.7	308	12	US-10-127-852A-100	Sequence 100, App
264	4	66.7	246	14	US-10-032-201B-188	Sequence 188, App	337	4	66.7	308	12	US-10-127-900A-100	Sequence 100, App
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266	4	66.7	247	9	US-09-815-242-13622	Sequence 13622, A	339	4	66.7	308	12	US-10-131-820A-100	Sequence 100, App
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270	4	66.7	249	16	US-10-437-963-200059	Sequence 200059, A	343	4	66.7	308	12	US-10-147-499-100	Sequence 100, App
271	4	66.7	250	9	US-09-738-626-4799	Sequence 4799, Ap	344	4	66.7	308	12	US-10-157-798-100	Sequence 100, App
272	4	66.7	250	14	US-10-017-161-1662	Sequence 1662, Ap	345	4	66.7	308	14	US-10-028-072-100	Sequence 100, App
273	4	66.7	251	12	US-10-282-122A-74141	Sequence 74141, A	346	4	66.7	308	14	US-10-121-049-100	Sequence 100, App
274	4	66.7	251	16	US-10-437-963-123072	Sequence 123072, A	347	4	66.7	308	14	US-10-123-904-100	Sequence 100, App
275	4	66.7	254	16	US-10-437-963-185711	Sequence 185711, A	348	4	66.7	308	14	US-10-140-470-100	Sequence 100, App
276	4	66.7	255	12	US-10-282-122A-51101	Sequence 51101, A	349	4	66.7	308	14	US-10-175-746-100	Sequence 100, App
277	4	66.7	257	14	US-10-080-170-217	Sequence 217, App	350	4	66.7	308	14	US-10-176-918-100	Sequence 100, App
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281	4	66.7	261	16	US-10-408-765A-1639	Sequence 1639, Ap	354	4	66.7	308	14	US-10-142-431-100	Sequence 100, App
282	4	66.7	261	16	US-10-437-963-172905	Sequence 172905, A	355	4	66.7	308	14	US-10-143-114-100	Sequence 100, App
283	4	66.7	263	12	US-10-424-599-189338	Sequence 189338, A	356	4	66.7	308	14	US-10-140-002-100	Sequence 100, App
284	4	66.7	263	16	US-10-437-963-145396	Sequence 145396, A	357	4	66.7	308	14	US-10-142-419-100	Sequence 100, App
285	4	66.7	267	15	US-10-369-493-7929	Sequence 7929, Ap	358	4	66.7	308	14	US-10-123-263-100	Sequence 100, App
286	4	66.7	272	9	US-09-949-200B-1	Sequence 1, Appli	359	4	66.7	308	14	US-10-142-423-100	Sequence 100, App
287	4	66.7	273	12	US-10-282-122A-65381	Sequence 65381, A	360	4	66.7	308	14	US-10-121-050-100	Sequence 100, App
288	4	66.7	273	12	US-10-282-122A-60805	Sequence 60805, A	361	4	66.7	308	14	US-10-141-755-100	Sequence 100, App
289	4	66.7	276	12	US-10-424-599-143673	Sequence 143673, A	362	4	66.7	308	14	US-10-143-032-100	Sequence 100, App
290	4	66.7	279	16	US-10-437-963-201282	Sequence 201282, A	363	4	66.7	308	14	US-10-123-108-100	Sequence 100, App
291	4	66.7	280	9	US-09-712-363-283	Sequence 371, App	364	4	66.7	308	14	US-10-123-236-100	Sequence 100, App
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295	4	66.7	280	14	US-10-219-810-39	Sequence 39, Appli	368	4	66.7	308	14	US-10-121-045-100	Sequence 100, App
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298	4	66.7	281	14	US-10-051-681A-10	Sequence 10, Appli	371	4	66.7	308	14	US-10-124-819-100	Sequence 100, App
299	4	66.7	284	14	US-10-127-032-127	Sequence 127, App	372	4	66.7	308	14	US-10-124-822-100	Sequence 100, App
300	4	66.7	285	16	US-10-408-765A-2728	Sequence 2728, Ap	373	4	66.7	308	14	US-10-140-925-100	Sequence 100, App
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306	4	66.7	293	12	US-10-425-114-61999	Sequence 61999, A	379	4	66.7	308	14	US-10-127-839A-100	Sequence 100, App
307	4	66.7	293	14	US-10-306-762-178	Sequence 178, App	380	4	66.7	308	14	US-10-127-901A-100	Sequence 100, App

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382	4	66.7	308	14	US-10-131-813A-100	Sequence 100, App	455	4	66.7	308	14	US-10-127-827A-100	Sequence 100, App
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397	4	66.7	308	14	US-10-121-047-100	Sequence 100, App	470	4	66.7	308	14	US-10-131-817A-100	Sequence 100, App
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415	4	66.7	308	14	US-10-127-838B-100	Sequence 100, App	488	4	66.7	308	14	US-10-146-726-100	Sequence 100, App
416	4	66.7	308	14	US-10-127-842A-100	Sequence 100, App	489	4	66.7	308	14	US-10-146-727-100	Sequence 100, App
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423	4	66.7	308	14	US-10-127-853A-100	Sequence 100, App	496	4	66.7	308	14	US-10-141-698-100	Sequence 100, App
424	4	66.7	308	14	US-10-127-854A-100	Sequence 100, App	497	4	66.7	308	14	US-10-141-702-100	Sequence 100, App
425	4	66.7	308	14	US-10-128-684A-100	Sequence 100, App	498	4	66.7	308	14	US-10-141-702-100	Sequence 100, App
426	4	66.7	308	14	US-10-128-686A-100	Sequence 100, App	499	4	66.7	308	14	US-10-141-702-100	Sequence 100, App
427	4	66.7	308	14	US-10-128-690A-100	Sequence 100, App	500	4	66.7	308	14	US-10-142-421-100	Sequence 100, App
428	4	66.7	308	14	US-10-128-691A-100	Sequence 100, App	501	4	66.7	308	14	US-10-142-432-100	Sequence 100, App
429	4	66.7	308	14	US-10-131-819A-100	Sequence 100, App	502	4	66.7	308	14	US-10-142-432-100	Sequence 100, App
430	4	66.7	308	14	US-10-131-829A-100	Sequence 100, App	503	4	66.7	308	14	US-10-142-767-100	Sequence 100, App
431	4	66.7	308	14	US-10-131-836A-100	Sequence 100, App	504	4	66.7	308	14	US-10-143-033-100	Sequence 100, App
432	4	66.7	308	14	US-10-146-729-100	Sequence 100, App	505	4	66.7	308	14	US-10-143-033-100	Sequence 100, App
433	4	66.7	308	14	US-10-146-791-100	Sequence 100, App	506	4	66.7	308	14	US-10-143-033-100	Sequence 100, App
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435	4	66.7	308	14	US-10-147-508-100	Sequence 100, App	508	4	66.7	308	14	US-10-145-628-100	Sequence 100, App
436	4	66.7	308	14	US-10-147-512-100	Sequence 100, App	509	4	66.7	308	14	US-10-145-748-100	Sequence 100, App
437	4	66.7	308	14	US-10-175-735-100	Sequence 100, App	510	4	66.7	308	14	US-10-145-748-100	Sequence 100, App
438	4	66.7	308	14	US-10-121-050-100	Sequence 100, App	511	4	66.7	308	14	US-10-145-823-100	Sequence 100, App
439	4	66.7	308	14	US-10-121-056-100	Sequence 100, App	512	4	66.7	308	14	US-10-145-823-100	Sequence 100, App
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441	4	66.7	308	14	US-10-123-235-100	Sequence 100, App	514	4	66.7	308	14	US-10-146-725-100	Sequence 100, App
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446	4	66.7	308	14	US-10-123-905-100	Sequence 100, App	519	4	66.7	308	14	US-10-147-509-100	Sequence 100, App
447	4	66.7	308	14	US-10-123-907-100	Sequence 100, App	520	4	66.7	308	14	US-10-147-510-100	Sequence 100, App
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449	4	66.7	308	14	US-10-125-928A-100	Sequence 100, App	522	4	66.7	308	14	US-10-147-529-100	Sequence 100, App
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453	4	66.7	308	14	US-10-127-824A-100	Sequence 100, App	526	4	66.7	308	14	US-10-137-870-100	Sequence 100, App

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533	4	66.7	308	14	US-10-158-783-100	Sequence 100, App	606	4	66.7	308	14	US-10-152-406-100	Sequence 100, App
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536	4	66.7	308	14	US-10-140-022-100	Sequence 100, App	609	4	66.7	308	14	US-10-157-799-100	Sequence 100, App
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556	4	66.7	308	14	US-10-142-887-100	Sequence 100, App	629	4	66.7	308	14	US-10-142-762-100	Sequence 100, App
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572	4	66.7	308	14	US-10-145-818-100	Sequence 100, App	645	4	66.7	308	14	US-10-306-762-167	Sequence 167, App
573	4	66.7	308	14	US-10-145-820-100	Sequence 100, App	646	4	66.7	308	14	US-10-306-762-167	Sequence 167, App
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695	4	66.7	308	14	US-10-121-063-100	Sequence 100, App	768	4	66.7	313	14	US-10-306-762-109
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969 4 66.7 483 16 US-10-745-034-16 Sequence 16, Appl
970 4 66.7 484 9 US-09-815-242-10457 Sequence 10457, A
971 4 66.7 484 12 US-10-282-1228-56797 Sequence 56797, A
972 4 66.7 486 15 US-10-369-493-7605 Sequence 7605, Ap
973 4 66.7 486 16 US-10-437-963-118754 Sequence 118754, A
974 4 66.7 489 10 US-09-888-320-2 Sequence 2, Appl
975 4 66.7 494 14 US-10-230-026-38 Sequence 38, Appl
976 4 66.7 495 11 US-09-833-245-302 Sequence 302, App
977 4 66.7 495 12 US-10-282-1228-68228 Sequence 68228, A
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993 4 66.7 516 16 US-10-437-963-193217 Sequence 193217, A
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995 4 66.7 523 14 US-10-029-495-3 Sequence 3, Appl
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997 4 66.7 524 15 US-10-369-493-7544 Sequence 7544, Ap
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ALIGNMENTS

RESULT 1
US-09-847-946A-41
; Sequence 41, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
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; PRIOR FILING DATE: 2000-05-02
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; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
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Query Match 100.0%; Score 6; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-847-946A-73
; Sequence 73, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
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; OTHER INFORMATION: sequence
US-09-847-946A-73
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Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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; Sequence 77, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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RESULT 4

US-09-847-946A-70
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; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
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; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 70
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-70

Query Match 100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 3 ADWSWA 8

RESULT 5

US-09-847-946A-78
; Sequence 78, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence
US-09-847-946A-78

Query Match 100.0%; Score 6; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 6

US-09-847-946A-69
; Sequence 69, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-69

Query Match 100.0%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
Db 1 ADWSWA 6

RESULT 7

US-09-847-946A-72
; Sequence 72, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 9
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-72
  Query Match      100.0%; Score 6; DB 10; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.2e+06;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
   |||||
Db 1 ADWSWA 6

RESULT 8
US-09-847-946A-75
; Sequence 75, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 75
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-75
  Query Match      100.0%; Score 6; DB 10; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.2e+06;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
   |||||
Db 3 ADWSWA 8

RESULT 9
US-09-847-946A-76
; Sequence 76, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 76
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-76
  Query Match      100.0%; Score 6; DB 10; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.2e+06;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
   |||||
Db 2 ADWSWA 7

RESULT 10
US-09-847-946A-71
; Sequence 71, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-71
  Query Match      100.0%; Score 6; DB 10; Length 10;
  Best Local Similarity 100.0%; Pred. No. 0.31;
  Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
   |||||
Db 2 ADWSWA 7

RESULT 11
US-09-847-946A-74
; Sequence 74, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
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; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-74

Query Match      100.0%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8

RESULT 12
US-09-847-946A-68
; Sequence 68, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-68

Query Match      100.0%; Score 6; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSWA 6
Db      3 ADWSWA 8

RESULT 13
US-09-847-940B-4
; Sequence 4, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-4

Query Match      83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      1 ADWSW 5

RESULT 14
US-09-847-940B-5
; Sequence 5, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-5

Query Match      83.3%; Score 5; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      2 DWSWA 6

RESULT 15
US-09-847-946A-4
; Sequence 4, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
```

```
;
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-4

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 16
US-09-847-946A-5
; Sequence 5, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-5

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 17
US-09-847-946A-39
; Sequence 39, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 39
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-39

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 18
US-09-847-946A-40
; Sequence 40, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-40

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 19
US-09-847-946A-51
; Sequence 51, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-51
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 51
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-51

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      1 ADWSW 5

RESULT 20
US-09-847-946A-62
; Sequence 62, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-62

Query Match      83.3%; Score 5; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      2 DWSWA 6

RESULT 21
US-09-847-946A-55
; Sequence 55, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
```

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; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-55

Query Match      83.3%; Score 5; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      1 ADWSW 5

RESULT 22
US-09-847-946A-66
; Sequence 66, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; US-09-847-946A-66

Query Match      83.3%; Score 5; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
Db      2 DWSWA 6

RESULT 23
US-09-847-946A-48
; Sequence 48, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 48
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-48

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSW 5
Db      3 ADMSW 7

RESULT 24
US-09-847-946A-56
; Sequence 56, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-56

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADMSW 5
Db      1 ADMSW 5

RESULT 25
US-09-847-946A-59
; Sequence 59, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 59
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-59

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

RESULT 26
US-09-847-946A-67
; Sequence 67, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 67
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-67

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

RESULT 27
US-09-847-946A-47
; Sequence 47, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 47
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match      83.3%; Score 5; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
Db      2 DWSWA 6

```

```
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-47

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 28
US-09-847-946A-50
; Sequence 50, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-50

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 1 ADWSW 5

RESULT 29
US-09-847-946A-53
; Sequence 53, Application US/09847946A
; Publication No. US20030054999A1
```

```
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-53

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 3 ADWSW 7

RESULT 30
US-09-847-946A-54
; Sequence 54, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-05-02
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-54

Query Match      83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 2 ADWSW 6

RESULT 31
```

Mon Jul 26 09:11:20 2004

US-09-847-946A-58
; Sequence 58, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-58

Query Match 83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 32
US-09-847-946A-61
; Sequence 61, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-61

Query Match 83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 33
US-09-847-946A-64
; Sequence 64, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-64

Query Match 83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 4 DWSWA 8

RESULT 34
US-09-847-946A-65
; Sequence 65, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-65

Query Match 83.3%; Score 5; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 DWSWA 6
      |||||
Db      3 DWSWA 7

RESULT 35
US-09-847-946A-49
; Sequence 49, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-49

Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
      |||||
Db      2 ADWSW 6

RESULT 36
US-09-847-946A-52
; Sequence 52, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-52

Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
      |||||
Db      2 ADWSW 6

RESULT 37
US-09-847-946A-57
; Sequence 57, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-57

Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      3 DWSWA 7

RESULT 38
US-09-847-946A-60
; Sequence 60, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-60
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Mon Jul 26 09:11:20 2004

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US-09-847-946A-60
Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      3 DWSWA 7

RESULT 39
US-09-847-946A-63
; Sequence 63, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-63

Query Match      83.3%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      4 DWSWA 8

RESULT 40
US-09-847-946A-46
; Sequence 46, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-46

Query Match      83.3%; Score 5; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
      |||||
Db      3 ADWSW 7

RESULT 41
US-10-424-599-199086
; Sequence 199086, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Xongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199086
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_2179C.1.pep
US-10-424-599-199086

Query Match      83.3%; Score 5; DB 12; Length 147;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSWA 6
      |||||
Db      75 DWSWA 79

RESULT 42
US-10-219-220-163
; Sequence 163, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-163

Query Match      83.3%; Score 5; DB 14; Length 174;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWSW 5
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; TYPE: PRT
; ORGANISM: C. hutchinsonii (23137247)
US-10-306-762-23

Query Match      83.3%; Score 5; DB 14; Length 312;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      171 ADWSW 175

RESULT 48
US-10-219-220-158
; Sequence 158, Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development
; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-219-220-158

Query Match      83.3%; Score 5; DB 14; Length 378;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      128 ADWSW 132

RESULT 49
US-10-171-311-234
; Sequence 234, Application US/10171311
; Publication No. US2003008270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 234
; LENGTH: 501
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-234

Query Match      83.3%; Score 5; DB 14; Length 501;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      387 ADWSW 391

RESULT 50
US-10-156-761-9070
; Sequence 9070, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9070
; LENGTH: 605
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9070

Query Match      83.3%; Score 5; DB 14; Length 605;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWSW 5
Db      556 ADWSW 560

Search completed: July 23, 2004, 13:32:44
Job time : 43 secs
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:25:00 ; Search time 19 Seconds
(without alignments)
16.303 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADMSWA 6

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
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- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTCUS COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	83.3	68	4	US-09-252-991A-18367
2	5	83.3	142	4	US-09-252-991A-31533
3	5	83.3	174	4	US-09-325-932A-163
4	5	83.3	225	4	US-09-325-932A-162
5	5	83.3	236	4	US-09-632-570-17
6	5	83.3	236	4	US-09-632-575-47
7	5	83.3	242	4	US-09-345-236B-3
8	5	83.3	378	4	US-09-325-932A-158
9	5	83.3	445	4	US-09-252-991A-22368
10	5	83.3	462	4	US-09-252-991A-21704
11	4	66.7	5	6	5217869-75
12	4	66.7	8	1	US-08-435-925C-9
13	4	66.7	9	1	US-08-435-925C-10
14	4	66.7	21	1	US-08-130-788A-246
15	4	66.7	21	1	US-08-383-474B-249
16	4	66.7	21	1	US-08-465-391A-246
17	4	66.7	21	2	US-08-464-538B-246
18	4	66.7	21	2	US-08-463-076E-303
19	4	66.7	21	4	US-09-428-082B-866
20	4	66.7	44	3	US-08-905-223-274
21	4	66.7	74	1	US-08-379-538-2
22	4	66.7	78	3	US-09-177-249-184
23	4	66.7	79	4	US-09-252-991A-27207
24	4	66.7	80	4	US-09-621-976-4160
25	4	66.7	84	3	US-09-251-372-4
26	4	66.7	84	4	US-09-811-241-4
27	4	66.7	84	4	US-09-252-991A-19040

28	4	66.7	95	4	US-09-252-991A-31932	Sequence 31932, A
29	4	66.7	100	1	US-08-241-853-28	Sequence 28, Appl
30	4	66.7	100	1	US-08-241-853-29	Sequence 29, Appl
31	4	66.7	100	2	US-08-850-917-28	Sequence 28, Appl
32	4	66.7	100	2	US-08-850-917-29	Sequence 29, Appl
33	4	66.7	106	2	US-08-585-585A-4	Sequence 4, Appl
34	4	66.7	106	2	US-08-249-037C-4	Sequence 4, Appl
35	4	66.7	106	2	US-08-788-622B-4	Sequence 4, Appl
36	4	66.7	106	3	US-08-788-621B-4	Sequence 4, Appl
37	4	66.7	109	1	US-08-477-270-20	Sequence 20, Appl
38	4	66.7	117	4	US-09-149-476-360	Sequence 360, App
39	4	66.7	121	4	US-09-673-395A-204	Sequence 204, App
40	4	66.7	125	4	US-09-543-681A-7177	Sequence 7177, Ap
41	4	66.7	138	4	US-09-252-991A-20154	Sequence 20154, A
42	4	66.7	163	4	US-09-257-583-13	Sequence 13, Appl
43	4	66.7	164	4	US-09-252-991A-23817	Sequence 23817, A
44	4	66.7	170	4	US-09-199-637A-339	Sequence 339, App
45	4	66.7	172	4	US-09-252-991A-23876	Sequence 23876, A
46	4	66.7	189	4	US-09-252-991A-17160	Sequence 17160, A
47	4	66.7	191	4	US-09-252-991A-28753	Sequence 28753, A
48	4	66.7	191	4	US-09-134-000C-3705	Sequence 3705, Ap
49	4	66.7	197	4	US-09-489-039A-12525	Sequence 12525, A
50	4	66.7	201	4	US-09-540-236-2208	Sequence 2208, Ap
51	4	66.7	213	3	US-09-268-364-4	Sequence 4, Appl
52	4	66.7	213	4	US-09-252-991A-27051	Sequence 27051, A
53	4	66.7	217	4	US-09-107-532A-6250	Sequence 6250, Ap
54	4	66.7	218	4	US-09-252-991A-22136	Sequence 22136, A
55	4	66.7	227	4	US-09-252-991A-28338	Sequence 28338, A
56	4	66.7	227	4	US-09-489-039A-8752	Sequence 8752, Ap
57	4	66.7	234	4	US-09-252-991A-26682	Sequence 26682, A
58	4	66.7	234	4	US-09-252-991A-28300	Sequence 28300, A
59	4	66.7	238	4	US-09-632-570-15	Sequence 15, Appl
60	4	66.7	238	4	US-09-632-575-45	Sequence 45, Appl
61	4	66.7	239	3	US-09-216-295-7	Sequence 7, Appl
62	4	66.7	239	3	US-09-216-295-15	Sequence 15, Appl
63	4	66.7	239	4	US-09-632-570-7	Sequence 7, Appl
64	4	66.7	239	4	US-09-632-575-37	Sequence 37, Appl
65	4	66.7	246	3	US-08-634-475-3	Sequence 3, Appl
66	4	66.7	246	4	US-09-709-791-3	Sequence 3, Appl
67	4	66.7	247	4	US-08-858-207A-300	Sequence 300, App
68	4	66.7	250	4	US-09-252-991A-19161	Sequence 19161, A
69	4	66.7	253	4	US-09-252-991A-29646	Sequence 29646, A
70	4	66.7	262	3	US-08-634-475-2	Sequence 2, Appl
71	4	66.7	262	4	US-09-709-791-2	Sequence 2, Appl
72	4	66.7	262	4	US-09-489-039A-10584	Sequence 10584, A
73	4	66.7	268	4	US-09-252-991A-31998	Sequence 31998, A
74	4	66.7	272	4	US-09-107-532A-5541	Sequence 5541, Ap
75	4	66.7	273	4	US-09-252-991A-19592	Sequence 19592, A
76	4	66.7	278	4	US-09-134-000C-3724	Sequence 3724, Ap
77	4	66.7	289	4	US-09-120-051D-49	Sequence 48, Appl
78	4	66.7	289	4	US-09-120-051D-49	Sequence 49, Appl
79	4	66.7	298	1	US-08-095-726-4	Sequence 4, Appl
80	4	66.7	298	1	US-08-096-043-4	Sequence 4, Appl
81	4	66.7	298	1	US-08-093-577-4	Sequence 4, Appl
82	4	66.7	298	1	US-08-096-623A-4	Sequence 4, Appl
83	4	66.7	303	4	US-09-252-991A-28605	Sequence 28605, A
84	4	66.7	306	3	US-09-457-046B-2	Sequence 2, Appl
85	4	66.7	307	1	US-08-095-726-2	Sequence 2, Appl
86	4	66.7	307	1	US-08-096-043-2	Sequence 2, Appl
87	4	66.7	307	1	US-08-093-577-2	Sequence 2, Appl
88	4	66.7	307	1	US-08-096-623A-2	Sequence 2, Appl
89	4	66.7	309	4	US-09-252-991A-27944	Sequence 27944, A
90	4	66.7	316	4	US-09-252-991A-22454	Sequence 22454, A
91	4	66.7	317	2	US-09-066-075-2	Sequence 2, Appl
92	4	66.7	317	2	US-08-518-615A-2	Sequence 2, Appl
93	4	66.7	317	3	US-08-951-889-2	Sequence 2, Appl
94	4	66.7	317	3	US-09-472-857-2	Sequence 2, Appl
95	4	66.7	317	4	US-09-118-637A-2	Sequence 2, Appl
96	4	66.7	319	4	US-09-134-000C-6357	Sequence 6357, Ap
97	4	66.7	324	4	US-09-252-991A-24664	Sequence 24664, A
98	4	66.7	327	4	US-09-252-991A-26846	Sequence 26846, A
99	4	66.7	331	4	US-09-252-991A-18772	Sequence 18772, A
100	4	66.7	333	4	US-09-107-532A-4041	Sequence 4041, Ap

101	4	66.7	337	3	US-09-320-878-15	Sequence 15, Appl	174	4	66.7	715	3	US-08-458-731-10	Sequence 10, Appl
102	4	66.7	337	3	US-09-105-537-14	Sequence 14, Appl	175	4	66.7	715	3	US-08-149-223A-10	Sequence 10, Appl
103	4	66.7	337	4	US-09-141-908-17	Sequence 17, Appl	176	4	66.7	716	2	US-08-484-993B-14	Sequence 14, Appl
104	4	66.7	337	4	US-09-657-440-15	Sequence 15, Appl	177	4	66.7	716	2	US-08-484-158B-14	Sequence 14, Appl
105	4	66.7	345	4	US-09-134-000C-6382	Sequence 6382, Ap	178	4	66.7	716	2	US-08-484-568A-14	Sequence 14, Appl
106	4	66.7	348	1	US-07-989-845-2	Sequence 2, Appli	179	4	66.7	716	2	US-08-480-150A-14	Sequence 14, Appl
107	4	66.7	348	4	US-09-118-637A-4	Sequence 4, Appli	180	4	66.7	716	3	US-08-458-731-14	Sequence 14, Appl
108	4	66.7	348	5	PCT-US93-11298-2	Sequence 2, Appli	181	4	66.7	716	3	US-08-149-223A-14	Sequence 14, Appl
109	4	66.7	351	4	US-09-252-991A-25097	Sequence 25097, A	182	4	66.7	717	1	US-08-435-925C-2	Sequence 2, Appli
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111	4	66.7	358	4	US-09-252-991A-16785	Sequence 16785, A	184	4	66.7	730	1	US-07-846-181-5	Sequence 5, Appli
112	4	66.7	360	4	US-09-509-902A-9	Sequence 9, Appli	185	4	66.7	730	1	US-07-845-989-5	Sequence 5, Appli
113	4	66.7	389	4	US-09-252-991A-32389	Sequence 32389, A	186	4	66.7	730	1	US-09-252-991A-30246	Sequence 30246, A
114	4	66.7	404	4	US-09-266-965-103	Sequence 103, App	187	4	66.7	735	2	US-08-887-518-3	Sequence 3, Appli
115	4	66.7	408	4	US-09-489-039A-12523	Sequence 12523, A	188	4	66.7	745	2	US-09-023-321-3	Sequence 3, Appli
116	4	66.7	410	4	US-09-540-236-3584	Sequence 3584, Ap	189	4	66.7	745	2	US-08-890-853-4	Sequence 4, Appli
117	4	66.7	416	4	US-09-540-236-3565	Sequence 6, Appli	190	4	66.7	745	2	US-09-032-475-3	Sequence 3, Appli
118	4	66.7	421	4	US-09-322-478-6	Sequence 22564, A	191	4	66.7	745	2	US-09-032-475-3	Sequence 4, Appli
119	4	66.7	429	4	US-09-252-991A-22564	Sequence 68, Appl	192	4	66.7	745	2	US-09-099-125A-4	Sequence 4, Appli
120	4	66.7	429	4	US-08-311-731A-68	Sequence 87, Appl	193	4	66.7	745	3	US-09-032-476-4	Sequence 4, Appli
121	4	66.7	433	3	US-08-691-563C-87	Sequence 87, Appl	194	4	66.7	745	3	US-08-890-854-4	Sequence 4, Appli
122	4	66.7	433	4	US-09-374-766-87	Sequence 87, Appl	195	4	66.7	745	3	US-09-023-324-4	Sequence 4, Appli
123	4	66.7	433	4	US-08-979-847B-81	Sequence 81, Appl	196	4	66.7	745	3	US-09-168-629-2	Sequence 2, Appli
124	4	66.7	438	4	US-09-252-991A-31307	Sequence 31307, A	197	4	66.7	745	3	US-08-310-820-10	Sequence 10, Appl
125	4	66.7	439	3	US-09-457-046B-28	Sequence 28, Appl	198	4	66.7	745	3	US-08-810-131A-2	Sequence 2, Appli
126	4	66.7	440	4	US-09-543-681A-6033	Sequence 6033, Ap	199	4	66.7	745	4	US-09-109-986-4	Sequence 4, Appli
127	4	66.7	445	4	US-09-252-991A-20277	Sequence 20277, A	200	4	66.7	745	4	US-09-844-908-10	Sequence 10, Appl
128	4	66.7	454	4	US-09-531-857A-4	Sequence 4, Appli	201	4	66.7	745	4	US-09-868-758-3	Sequence 3, Appli
129	4	66.7	474	4	US-08-311-731A-318	Sequence 318, App	202	4	66.7	756	2	US-09-023-321-4	Sequence 2, Appli
130	4	66.7	476	4	US-09-489-039A-8358	Sequence 8358, Ap	203	4	66.7	756	2	US-08-890-853-2	Sequence 2, Appli
131	4	66.7	480	4	US-09-252-991A-17687	Sequence 17687, A	204	4	66.7	756	2	US-09-032-475-4	Sequence 4, Appli
132	4	66.7	483	4	US-09-310-463-16	Sequence 16, Appl	205	4	66.7	756	2	US-09-032-475-4	Sequence 2, Appli
133	4	66.7	487	4	US-08-842-248A-16	Sequence 25447, A	206	4	66.7	756	2	US-09-032-475-4	Sequence 4, Appli
134	4	66.7	487	4	US-09-252-991A-25447	Sequence 8887, Ap	207	4	66.7	756	2	US-09-099-125A-2	Sequence 2, Appli
135	4	66.7	503	4	US-09-489-039A-8887	Sequence 8, Appli	208	4	66.7	756	3	US-09-099-125A-2	Sequence 2, Appli
136	4	66.7	506	4	US-09-215-694-8	Sequence 23066, A	209	4	66.7	756	3	US-09-032-476-2	Sequence 2, Appli
137	4	66.7	509	4	US-09-252-991A-23066	Sequence 20470, A	210	4	66.7	756	3	US-09-032-476-2	Sequence 2, Appli
138	4	66.7	526	2	US-08-853-401-3	Sequence 3, Appli	211	4	66.7	756	3	US-08-890-854-2	Sequence 2, Appli
139	4	66.7	542	4	US-09-252-991A-29987	Sequence 29987, A	212	4	66.7	756	3	US-09-168-629-15	Sequence 15, Appl
140	4	66.7	543	3	US-09-155-768-4	Sequence 4, Appli	213	4	66.7	756	3	US-09-109-986-2	Sequence 2, Appli
141	4	66.7	556	4	US-09-198-452A-596	Sequence 596, App	214	4	66.7	756	4	US-09-844-908-9	Sequence 9, Appli
142	4	66.7	570	4	US-09-565-501A-104	Sequence 104, App	215	4	66.7	756	4	US-09-109-986-2	Sequence 9, Appli
143	4	66.7	570	4	US-09-639-206A-104	Sequence 104, App	216	4	66.7	756	4	US-09-868-758-4	Sequence 4, Appli
144	4	66.7	570	4	US-09-874-923-104	Sequence 104, App	217	4	66.7	756	4	US-09-328-352-5942	Sequence 5, Appli
145	4	66.7	578	4	US-08-635-552A-2	Sequence 2, Appli	218	4	66.7	783	2	US-08-545-562A-5	Sequence 2, Appli
146	4	66.7	581	4	US-09-252-991A-25414	Sequence 25414, A	219	4	66.7	802	4	US-09-632-098-2	Sequence 2, Appli
147	4	66.7	583	4	US-08-673-499A-3	Sequence 3, Appli	220	4	66.7	826	4	US-09-134-000C-4999	Sequence 4999, Ap
148	4	66.7	583	4	US-08-812-008-3	Sequence 3, Appli	221	4	66.7	826	4	US-09-543-681A-8171	Sequence 8171, Ap
149	4	66.7	586	3	US-09-964-268-3	Sequence 3, Appli	222	4	66.7	951	4	Sequence 4456, Ap	Sequence 4456, Ap
150	4	66.7	586	4	US-09-105-254-3	Sequence 10369, A	223	4	66.7	951	4	Sequence 30672, A	Sequence 30672, A
151	4	66.7	594	4	US-09-489-039A-10369	Sequence 2, Appli	224	4	66.7	951	4	Sequence 6, Appli	Sequence 6, Appli
152	4	66.7	594	3	US-09-135-232-2	Sequence 2, Appli	225	4	66.7	968	4	Sequence 19, Appl	Sequence 19, Appl
153	4	66.7	596	3	US-09-863-549-2	Sequence 2, Appli	226	4	66.7	971	3	Sequence 4, Appli	Sequence 4, Appli
154	4	66.7	604	2	US-08-756-317-6	Sequence 6, Appli	227	4	66.7	982	2	Sequence 16, Appl	Sequence 16, Appl
155	4	66.7	606	4	US-09-618-425-5	Sequence 5, Appli	228	4	66.7	983	1	Sequence 10, Appl	Sequence 10, Appl
156	4	66.7	606	4	US-09-618-425-5	Sequence 5, Appli	229	4	66.7	983	1	Sequence 21, Appl	Sequence 21, Appl
157	4	66.7	608	4	US-09-489-039A-13204	Sequence 47, Appl	230	4	66.7	983	2	Sequence 10, Appl	Sequence 10, Appl
158	4	66.7	616	3	US-09-136-574A-47	Sequence 13204, A	231	4	66.7	983	3	Sequence 21, Appl	Sequence 21, Appl
159	4	66.7	626	4	US-09-252-991A-21504	Sequence 21504, A	232	4	66.7	983	3	Sequence 10, Appl	Sequence 10, Appl
160	4	66.7	626	4	US-09-800-729-95	Sequence 95, Appl	233	4	66.7	983	3	Sequence 21, Appl	Sequence 21, Appl
161	4	66.7	630	4	US-09-107-532A-6830	Sequence 6830, Ap	234	4	66.7	996	4	Sequence 10, Appl	Sequence 10, Appl
162	4	66.7	670	4	US-09-252-991A-22079	Sequence 22079, A	235	4	66.7	996	4	Sequence 21, Appl	Sequence 21, Appl
163	4	66.7	671	3	US-09-121-321-16	Sequence 16, Appl	236	4	66.7	1001	1	Sequence 21, Appl	Sequence 21, Appl
164	4	66.7	671	3	US-08-933-803A-16	Sequence 2, Appli	237	4	66.7	1001	1	Sequence 123, App	Sequence 123, App
165	4	66.7	677	3	US-08-836-567-2	Sequence 2, Appli	238	4	66.7	1001	1	Sequence 6, Appli	Sequence 6, Appli
166	4	66.7	677	4	US-09-606-304-2	Sequence 2, Appli	239	4	66.7	1036	3	Sequence 2, Appli	Sequence 2, Appli
167	4	66.7	689	3	US-09-177-243-2	Sequence 2, Appli	240	4	66.7	1036	3	Sequence 4, Appli	Sequence 4, Appli
168	4	66.7	689	3	US-09-061-769A-2	Sequence 2, Appli	241	4	66.7	1036	3	Sequence 4, Appli	Sequence 4, Appli
169	4	66.7	700	2	US-07-862-588B-2	Sequence 2, Appli	242	4	66.7	1043	4	Sequence 32210, A	Sequence 32210, A
170	4	66.7	715	2	US-08-484-993B-10	Sequence 10, Appl	243	4	66.7	1047	2	Sequence 6186, Ap	Sequence 6186, Ap
171	4	66.7	715	2	US-08-484-158B-10	Sequence 10, Appl	244	4	66.7	1074	3	Sequence 2, Appli	Sequence 2, Appli
172	4	66.7	715	2	US-08-484-596A-10	Sequence 10, Appl	245	4	66.7	1074	3	Sequence 2, Appli	Sequence 2, Appli
173	4	66.7	715	2	US-08-480-150A-10	Sequence 10, Appl	246	4	66.7	1074	4	Sequence 2, Appli	Sequence 2, Appli

247	4	66.7	1086	4	US-09-252-991A-25051	Sequence 25051, A	320	3	50.0	8	3	US-09-082-279B-1480	Sequence 1480, Ap
248	4	66.7	1097	1	US-07-943-843-6	Sequence 6, Appl	321	3	50.0	8	3	US-09-082-279B-1482	Sequence 1482, Ap
249	4	66.7	1097	1	US-08-347-003-6	Sequence 6, Appl	322	3	50.0	8	3	US-09-082-279B-1494	Sequence 1494, Ap
250	4	66.7	1170	4	US-09-638-524A-2	Sequence 2, Appl	323	3	50.0	8	3	US-09-082-279B-1499	Sequence 1499, Ap
251	4	66.7	1180	4	US-09-252-991A-32464	Sequence 32464, A	324	3	50.0	8	3	US-09-082-279B-1502	Sequence 1502, Ap
252	4	66.7	1197	3	US-08-836-567-12	Sequence 12, Appl	325	3	50.0	8	3	US-09-082-279B-1504	Sequence 1504, Ap
253	4	66.7	1197	3	US-08-606-304-12	Sequence 12, Appl	326	3	50.0	8	3	US-09-082-279B-1506	Sequence 1506, Ap
254	4	66.7	1230	2	US-08-968-542C-35	Sequence 35, Appl	327	3	50.0	8	3	US-09-082-279B-1507	Sequence 1507, Ap
255	4	66.7	1230	4	US-09-554-467A-35	Sequence 35, Appl	328	3	50.0	8	3	US-09-082-279B-1511	Sequence 1511, Ap
256	4	66.7	1269	4	US-09-252-991A-23150	Sequence 23150, A	329	3	50.0	8	4	US-09-043-731-4	Sequence 4, Appl
257	4	66.7	1272	4	US-09-543-671A-5732	Sequence 5732, Ap	330	3	50.0	8	4	US-09-315-304B-1629	Sequence 1629, Ap
258	4	66.7	1426	3	US-08-136-574A-43	Sequence 43, Appl	331	3	50.0	8	4	US-09-315-304B-1630	Sequence 1630, Ap
259	4	66.7	1674	2	US-08-968-542C-12	Sequence 12, Appl	332	3	50.0	8	4	US-09-315-304B-1631	Sequence 1631, Ap
260	4	66.7	1674	4	US-09-554-467A-12	Sequence 12, Appl	333	3	50.0	8	4	US-09-315-304B-1632	Sequence 1632, Ap
261	4	66.7	1751	4	US-09-136-574A-44	Sequence 44, Appl	334	3	50.0	8	4	US-09-315-304B-1633	Sequence 1633, Ap
262	4	66.7	1841	2	US-08-804-227C-6	Sequence 6, Appl	335	3	50.0	8	4	US-09-315-304B-1634	Sequence 1634, Ap
263	4	66.7	2482	4	US-09-252-991A-16967	Sequence 16967, A	336	3	50.0	8	4	US-09-315-304B-1636	Sequence 1636, Ap
264	4	66.7	3168	4	US-09-489-039A-14067	Sequence 14067, A	337	3	50.0	8	4	US-09-315-304B-1648	Sequence 1648, Ap
265	4	66.7	3782	3	US-09-105-537-4	Sequence 4, Appl	338	3	50.0	8	4	US-09-315-304B-1653	Sequence 1653, Ap
266	4	66.7	4630	4	US-09-091-609-2	Sequence 2, Appl	339	3	50.0	8	4	US-09-315-304B-1656	Sequence 1656, Ap
267	4	66.7	5215	3	US-09-105-537-2	Sequence 2, Appl	340	3	50.0	8	4	US-09-315-304B-1658	Sequence 1658, Ap
268	3	50.0	4	2	US-08-478-386A-7	Sequence 7, Appl	341	3	50.0	8	4	US-09-315-304B-1660	Sequence 1660, Ap
269	3	50.0	4	2	US-08-292-597-7	Sequence 7, Appl	342	3	50.0	8	4	US-09-315-304B-1665	Sequence 1665, Ap
270	3	50.0	4	2	US-08-388-553-7	Sequence 7, Appl	343	3	50.0	8	4	US-08-439-157-5	Sequence 5, Appl
271	3	50.0	4	2	US-08-473-985-7	Sequence 7, Appl	344	3	50.0	8	4	US-08-439-157-34	Sequence 34, Appl
272	3	50.0	4	2	US-08-483-898-7	Sequence 7, Appl	345	3	50.0	8	4	US-08-439-157-75	Sequence 75, Appl
273	3	50.0	4	3	US-08-689-421-9	Sequence 9, Appl	346	3	50.0	8	4	US-09-437-895-5	Sequence 5, Appl
274	3	50.0	4	3	US-09-087-716-7	Sequence 7, Appl	347	3	50.0	8	4	US-09-437-895-34	Sequence 34, Appl
275	3	50.0	4	3	US-08-297-395-68	Sequence 68, Appl	348	3	50.0	8	4	US-09-437-895-75	Sequence 75, Appl
276	3	50.0	4	3	US-08-237-395-71	Sequence 71, Appl	349	3	50.0	8	4	US-08-469-260A-528	Sequence 528, App
277	3	50.0	4	3	US-08-297-395-74	Sequence 74, Appl	350	3	50.0	8	4	US-08-488-446-528	Sequence 528, App
278	3	50.0	4	3	US-08-157-753-7	Sequence 7, Appl	351	3	50.0	8	4	US-09-834-784-1475	Sequence 1475, Ap
279	3	50.0	4	3	US-09-157-230-7	Sequence 7, Appl	352	3	50.0	8	4	US-09-834-784-1476	Sequence 1476, Ap
280	3	50.0	4	3	US-09-087-811-7	Sequence 7, Appl	353	3	50.0	8	4	US-09-834-784-1477	Sequence 1477, Ap
281	3	50.0	4	3	US-09-156-855-7	Sequence 7, Appl	354	3	50.0	8	4	US-09-834-784-1479	Sequence 1479, Ap
282	3	50.0	4	3	US-09-158-010-7	Sequence 7, Appl	355	3	50.0	8	4	US-09-834-784-1480	Sequence 1480, Ap
283	3	50.0	4	3	US-09-087-647-7	Sequence 7, Appl	356	3	50.0	8	4	US-09-834-784-1482	Sequence 1482, Ap
284	3	50.0	4	3	US-09-389-528-9	Sequence 9, Appl	357	3	50.0	8	4	US-09-834-784-1494	Sequence 1494, Ap
285	3	50.0	4	3	US-09-181-827A-9	Sequence 9, Appl	358	3	50.0	8	4	US-09-834-784-1499	Sequence 1499, Ap
286	3	50.0	4	4	US-09-302-629-7	Sequence 7, Appl	359	3	50.0	8	4	US-09-834-784-1502	Sequence 1502, Ap
287	3	50.0	5	2	US-08-684-687-7	Sequence 7, Appl	360	3	50.0	8	4	US-09-834-784-1504	Sequence 1504, Ap
288	3	50.0	5	2	US-08-981-122-55	Sequence 55, Appl	361	3	50.0	8	4	US-09-834-784-1506	Sequence 1506, Ap
289	3	50.0	5	6	5217869-56	Patent No. 5217869	362	3	50.0	8	4	US-09-834-784-1507	Sequence 1507, Ap
290	3	50.0	6	1	US-08-596-116A-3	Sequence 3, Appl	363	3	50.0	8	4	US-09-834-784-1511	Sequence 1511, Ap
291	3	50.0	6	1	US-08-596-116A-6	Sequence 6, Appl	364	3	50.0	8	4	US-08-467-344A-528	Sequence 528, App
292	3	50.0	6	1	US-08-596-116A-9	Sequence 9, Appl	365	3	50.0	8	4	US-09-350-641C-1630	Sequence 1630, Ap
293	3	50.0	6	1	US-08-596-116A-13	Sequence 13, Appl	366	3	50.0	8	4	US-09-350-641C-1631	Sequence 1631, Ap
294	3	50.0	6	1	US-08-596-116A-16	Sequence 16, Appl	367	3	50.0	8	4	US-09-350-641C-1632	Sequence 1632, Ap
295	3	50.0	6	1	US-08-596-116A-21	Sequence 21, Appl	368	3	50.0	8	4	US-09-350-641C-1634	Sequence 1634, Ap
296	3	50.0	6	1	US-08-596-116A-26	Sequence 26, Appl	369	3	50.0	8	4	US-09-350-641C-1635	Sequence 1635, Ap
297	3	50.0	6	1	US-08-596-116A-29	Sequence 29, Appl	370	3	50.0	8	4	US-09-350-641C-1637	Sequence 1637, Ap
298	3	50.0	6	1	US-08-596-116A-33	Sequence 33, Appl	371	3	50.0	8	4	US-09-350-641C-1649	Sequence 1649, Ap
299	3	50.0	6	1	US-08-596-116A-42	Sequence 42, Appl	372	3	50.0	8	4	US-09-350-641C-1654	Sequence 1654, Ap
300	3	50.0	6	4	US-08-981-957D-9	Sequence 9, Appl	373	3	50.0	8	4	US-09-350-641C-1657	Sequence 1657, Ap
301	3	50.0	6	4	US-08-871-561-28	Sequence 28, Appl	374	3	50.0	8	4	US-09-350-641C-1659	Sequence 1659, Ap
302	3	50.0	6	4	US-09-301-593-67	Sequence 67, Appl	375	3	50.0	8	4	US-09-350-641C-1661	Sequence 1661, Ap
303	3	50.0	6	4	US-09-321-932B-28	Sequence 28, Appl	376	3	50.0	8	4	US-09-350-641C-1662	Sequence 1662, Ap
304	3	50.0	6	6	5217891-1	Patent No. 5217891	377	3	50.0	8	4	US-09-350-641C-1666	Sequence 1666, Ap
305	3	50.0	7	1	US-07-801-812A-24	Sequence 24, Appl	378	3	50.0	9	3	US-08-159-339A-340	Sequence 340, App
306	3	50.0	7	1	US-08-173-510B-77	Sequence 77, Appl	379	3	50.0	9	3	US-09-258-754-350	Sequence 350, App
307	3	50.0	7	1	US-08-462-661A-46	Sequence 46, Appl	380	3	50.0	9	3	US-09-042-107-350	Sequence 350, App
308	3	50.0	7	1	US-08-487-568-24	Sequence 24, Appl	381	3	50.0	9	3	US-09-510-738A-45	Sequence 45, Appl
309	3	50.0	7	1	US-08-458-218-75	Sequence 75, Appl	382	3	50.0	9	3	US-09-510-738A-105	Sequence 105, App
310	3	50.0	7	2	US-08-450-497-77	Sequence 77, Appl	383	3	50.0	9	3	US-09-510-738A-106	Sequence 106, App
311	3	50.0	7	6	531859-62	Patent No. 531859	384	3	50.0	9	3	US-09-510-738A-121	Sequence 121, App
312	3	50.0	8	3	US-08-336-553A-5	Sequence 5, Appl	385	3	50.0	9	4	US-08-817-441-22	Sequence 22, Appl
313	3	50.0	8	3	US-08-336-553A-34	Sequence 34, Appl	386	3	50.0	9	4	US-09-861-966-45	Sequence 45, Appl
314	3	50.0	8	3	US-08-336-553A-75	Sequence 75, Appl	387	3	50.0	9	4	US-09-861-966-105	Sequence 105, App
315	3	50.0	8	3	US-08-444-818-377	Sequence 377, App	388	3	50.0	9	4	US-09-861-966-106	Sequence 106, App
316	3	50.0	8	3	US-09-082-279B-1475	Sequence 1475, Ap	389	3	50.0	9	4	US-09-861-966-121	Sequence 121, App
317	3	50.0	8	3	US-08-082-279B-1476	Sequence 1476, Ap	390	3	50.0	9	4	US-09-311-784A-164	Sequence 164, App
318	3	50.0	8	3	US-08-082-279B-1477	Sequence 1477, Ap	391	3	50.0	9	4	US-09-311-784A-238	Sequence 238, App
319	3	50.0	8	3	US-09-082-279B-1479	Sequence 1479, Ap	392	3	50.0	9	4	US-09-311-784A-231	Sequence 231, App

393	3	50.0	9	4	US-09-311-784A-232	Sequence 232, App	466	3	50.0	19	1	US-08-290-448A-16	Sequence 16, Appl
394	3	50.0	9	4	US-09-311-784A-233	Sequence 233, App	467	3	50.0	19	1	US-08-290-448A-16	Sequence 16, Appl
395	3	50.0	9	4	US-09-722-250D-350	Sequence 350, App	468	3	50.0	19	1	US-08-471-033-25	Sequence 25, Appl
396	3	50.0	10	1	US-07-965-675-7	Sequence 7, Appli	469	3	50.0	19	1	US-08-484-635-104	Sequence 104, App
397	3	50.0	10	1	US-08-264-093-8	Sequence 8, Appli	470	3	50.0	19	1	US-08-175-069A-16	Sequence 16, Appl
398	3	50.0	10	1	US-08-290-448A-53	Sequence 53, Appl	471	3	50.0	19	2	US-08-484-631-104	Sequence 104, App
399	3	50.0	10	1	US-08-290-448A-53	Sequence 53, Appl	472	3	50.0	19	2	US-08-471-044-25	Sequence 25, Appl
400	3	50.0	10	1	US-08-175-069A-53	Sequence 53, Appl	473	3	50.0	19	2	US-08-463-483A-25	Sequence 25, Appl
401	3	50.0	10	1	US-08-726-464B-8	Sequence 8, Appli	474	3	50.0	19	2	US-08-471-046A-25	Sequence 25, Appl
402	3	50.0	10	2	US-08-726-464B-11	Sequence 11, Appl	475	3	50.0	19	2	US-08-470-566B-25	Sequence 25, Appl
403	3	50.0	10	3	US-08-159-339A-478	Sequence 478, App	476	3	50.0	19	2	US-08-827-570-104	Sequence 104, App
404	3	50.0	10	4	US-08-461-939B-53	Sequence 53, Appl	477	3	50.0	19	2	US-09-174-060-20	Sequence 20, Appl
405	3	50.0	10	4	US-08-464-000-53	Sequence 53, Appl	478	3	50.0	19	2	US-08-469-334-25	Sequence 25, Appl
406	3	50.0	10	4	US-09-790-497A-26	Sequence 26, Appl	479	3	50.0	19	3	US-09-300-529-25	Sequence 25, Appl
407	3	50.0	10	4	US-09-428-082B-37	Sequence 37, App	480	3	50.0	19	3	US-08-338-382-20	Sequence 20, Appl
408	3	50.0	10	5	PCT-US91-02342-61	Sequence 61, Appl	481	3	50.0	19	4	US-08-461-939B-16	Sequence 16, Appl
409	3	50.0	10	6	5198533-4	Sequence 61, Appl	482	3	50.0	19	4	US-08-464-000-16	Sequence 16, Appl
410	3	50.0	10	6	5217891-20	Patent No. 5217891	483	3	50.0	19	4	US-08-469-260A-432	Sequence 432, App
411	3	50.0	11	2	US-08-849-536A-16	Sequence 16, Appl	484	3	50.0	19	4	US-09-301-593-61	Sequence 61, Appl
412	3	50.0	11	3	US-09-183-217-9	Sequence 9, Appli	485	3	50.0	19	4	US-08-488-446-432	Sequence 432, App
413	3	50.0	11	3	US-08-836-075A-107	Sequence 107, App	486	3	50.0	19	4	US-08-467-344A-432	Sequence 432, App
414	3	50.0	11	3	US-08-836-075A-108	Sequence 108, App	487	3	50.0	19	4	US-09-097-055B-45	Sequence 45, Appl
415	3	50.0	11	3	US-08-836-075A-109	Sequence 109, App	488	3	50.0	19	4	US-09-097-055B-51	Sequence 51, Appl
416	3	50.0	11	3	US-08-836-075A-110	Sequence 110, App	489	3	50.0	19	4	US-09-829-855-232	Sequence 232, App
417	3	50.0	11	3	US-08-836-075A-117	Sequence 117, App	490	3	50.0	20	1	US-08-382-013A-38	Sequence 38, Appl
418	3	50.0	11	4	US-09-142-680-16	Sequence 16, Appl	491	3	50.0	20	1	US-08-241-054-88	Sequence 74, Appl
419	3	50.0	11	4	US-09-430-503-15	Sequence 15, Appl	492	3	50.0	20	1	US-08-390-156A-74	Sequence 4, Appli
420	3	50.0	12	2	US-08-146-028-26	Sequence 26, Appl	493	3	50.0	20	1	US-08-419-009-4	Sequence 68, Appl
421	3	50.0	12	3	US-08-603-024-9	Sequence 9, Appli	494	3	50.0	20	1	US-08-439-817-68	Sequence 88, Appl
422	3	50.0	12	3	US-08-723-425A-26	Sequence 26, Appl	495	3	50.0	20	1	US-08-485-508-88	Sequence 26, Appl
423	3	50.0	12	3	US-09-112-006-26	Sequence 26, Appl	496	3	50.0	20	2	US-08-484-530-26	Sequence 26, Appl
424	3	50.0	12	4	US-09-407-687-24	Sequence 24, Appl	497	3	50.0	20	2	US-08-827-618A-26	Sequence 26, Appl
425	3	50.0	12	4	US-09-051-380-8	Sequence 8, Appli	498	3	50.0	20	3	US-08-483-952A-26	Sequence 27, Appl
426	3	50.0	12	4	US-09-403-752A-93	Sequence 93, Appl	499	3	50.0	20	3	US-08-894-017-27	Sequence 1, Appli
427	3	50.0	12	4	US-09-576-824A-26	Sequence 26, Appl	500	3	50.0	20	4	US-08-464-496-1	Sequence 26, Appl
428	3	50.0	13	2	US-08-480-190-26	Sequence 26, Appl	501	3	50.0	20	4	US-08-476-501-26	Sequence 1, Appli
429	3	50.0	13	2	US-08-488-379-26	Sequence 26, Appl	502	3	50.0	20	4	US-09-161-939A-1	Sequence 9, Appli
430	3	50.0	13	2	US-08-727-688-20	Sequence 20, Appl	503	3	50.0	20	4	US-09-161-939A-9	Sequence 27, Appl
431	3	50.0	13	3	US-08-727-308-8	Sequence 8, Appli	504	3	50.0	20	4	US-09-456-474-27	Sequence 1, Appli
432	3	50.0	13	4	US-08-475-399A-26	Sequence 26, Appl	505	3	50.0	20	5	PCT-US92-07218-1	Sequence 3, Appli
433	3	50.0	13	5	PCT-US93-07545-26	Sequence 26, App	506	3	50.0	21	2	US-08-612-840A-3	Sequence 6, Appli
434	3	50.0	14	2	US-08-480-190-176	Sequence 176, App	507	3	50.0	21	4	US-09-508-803-3	Sequence 6, Appli
435	3	50.0	14	2	US-08-488-379-176	Sequence 176, App	508	3	50.0	22	1	US-07-933-469A-6	Sequence 6, Appli
436	3	50.0	14	3	US-08-782-997A-7	Sequence 7, Appli	509	3	50.0	22	1	US-08-250-310-6	Sequence 6, Appli
437	3	50.0	14	3	US-08-682-791B-2	Sequence 2, Appli	510	3	50.0	22	1	US-08-439-404-6	Sequence 6, Appli
438	3	50.0	14	4	US-08-218-369-6	Sequence 6, Appli	511	3	50.0	22	1	US-08-839-327-6	Sequence 6, Appli
439	3	50.0	14	4	US-09-413-611A-2	Sequence 2, Appli	512	3	50.0	22	3	US-09-340-781B-6	Sequence 884, App
440	3	50.0	14	4	US-08-475-399A-176	Sequence 176, App	513	3	50.0	22	4	US-09-205-258-884	Sequence 385, App
441	3	50.0	14	5	PCT-US93-07545-176	Sequence 176, App	514	3	50.0	23	4	US-08-905-223-385	Sequence 7, Appli
442	3	50.0	15	1	PCT-US95-03742-6	Sequence 6, Appli	515	3	50.0	23	4	US-08-951-034B-7	Sequence 12, Appl
443	3	50.0	15	1	US-08-551-128A-1	Sequence 1, Appli	516	3	50.0	24	3	US-08-895-474-12	Sequence 23, Appl
444	3	50.0	15	4	US-09-829-855-223	Sequence 23, App	517	3	50.0	24	4	US-08-905-054B-23	Sequence 248, App
445	3	50.0	15	5	PCT-US93-06751-5	Sequence 5, Appli	518	3	50.0	24	4	US-09-721-108-248	Sequence 249, App
446	3	50.0	15	5	PCT-US93-06751-37	Sequence 37, Appl	519	3	50.0	24	4	US-09-721-108-249	Sequence 250, App
447	3	50.0	16	1	US-08-321-625-53	Sequence 53, Appl	520	3	50.0	24	4	US-09-721-108-250	Sequence 23, Appl
448	3	50.0	16	1	US-08-321-625-80	Sequence 80, Appl	521	3	50.0	24	5	PCT-US92-07813-23	Sequence 155, App
449	3	50.0	16	3	US-09-181-083-53	Sequence 53, Appl	522	3	50.0	25	2	US-08-480-190-155	Sequence 155, App
450	3	50.0	16	3	US-09-181-083-80	Sequence 80, Appl	523	3	50.0	25	2	US-08-488-379-155	Sequence 17, Appl
451	3	50.0	16	4	US-09-330-914A-11	Sequence 11, Appl	524	3	50.0	25	2	US-08-997-080-17	Sequence 17, Appl
452	3	50.0	16	4	US-09-073-009-66	Sequence 66, Appl	525	3	50.0	25	2	US-08-997-162-17	Sequence 17, Appl
453	3	50.0	16	4	US-09-073-010-66	Sequence 66, Appl	526	3	50.0	25	3	US-08-873-370-17	Sequence 18, Appl
454	3	50.0	16	4	US-09-750-754-53	Sequence 53, Appl	527	3	50.0	25	3	US-08-948-378A-18	Sequence 18, Appl
455	3	50.0	16	4	US-09-750-754-80	Sequence 80, Appl	528	3	50.0	25	3	US-09-095-855-17	Sequence 17, Appl
456	3	50.0	17	1	US-09-025-769B-223	Sequence 223, App	529	3	50.0	25	3	US-09-169-425C-18	Sequence 18, Appl
457	3	50.0	18	1	US-08-487-568-41	Sequence 41, Appl	530	3	50.0	25	3	US-08-705-347A-17	Sequence 17, Appl
458	3	50.0	18	3	US-08-336-553A-53	Sequence 53, Appl	531	3	50.0	25	4	US-09-324-542-17	Sequence 4, Appli
459	3	50.0	18	3	US-08-336-553A-54	Sequence 54, Appl	532	3	50.0	25	4	US-09-302-329A-4	Sequence 17, Appl
460	3	50.0	18	3	US-08-909-954-12	Sequence 12, Appl	533	3	50.0	25	4	US-09-205-426-17	Sequence 17, Appl
461	3	50.0	18	4	US-08-439-157-53	Sequence 53, Appl	534	3	50.0	25	4	US-09-200-643-17	Sequence 1, Appli
462	3	50.0	18	4	US-08-439-157-54	Sequence 54, Appl	535	3	50.0	25	4	US-09-440-344-1	Sequence 155, App
463	3	50.0	18	4	US-09-437-895-53	Sequence 53, Appl	536	3	50.0	25	4	US-08-475-399A-155	Sequence 3, Appli
464	3	50.0	18	4	US-09-437-895-54	Sequence 54, Appl	537	3	50.0	25	4	US-09-692-064-3	
465	3	50.0	18	4	US-09-407-687-36	Sequence 36, Appl	538	3	50.0	25	4		

539	3	50.0	25	4	US-09-552-802B-43	Sequence 43, Appl	612	3	50.0	36	4	US-09-515-965A-1212	Sequence 1212, Ap
540	3	50.0	25	4	US-09-759-960-18	Sequence 18, Appl	613	3	50.0	36	4	US-09-350-641C-1051	Sequence 1051, Ap
541	3	50.0	25	4	US-09-084-303B-296	Sequence 296, Appl	614	3	50.0	36	4	US-09-350-641C-1212	Sequence 1212, Ap
542	3	50.0	25	4	US-09-667-319-4	Sequence 4, Appl	615	3	50.0	37	1	US-08-118-270-212	Sequence 212, Ap
543	3	50.0	25	5	PCT-US93-07545-155	Sequence 155, Appl	616	3	50.0	37	1	US-07-929-206-5	Sequence 5, Appl
544	3	50.0	26	4	US-08-525-539A-21	Sequence 21, Appl	617	3	50.0	37	1	US-07-929-206-6	Sequence 6, Appl
545	3	50.0	26	4	US-09-152-060-117	Sequence 117, Appl	618	3	50.0	37	1	US-07-929-206-8	Sequence 8, Appl
546	3	50.0	26	4	US-08-469-260A-191	Sequence 191, Appl	619	3	50.0	37	1	US-08-682-485A-14	Sequence 14, Appl
547	3	50.0	26	4	US-09-407-687-39	Sequence 39, Appl	620	3	50.0	37	1	US-08-682-485A-16	Sequence 16, Appl
548	3	50.0	26	4	US-08-488-446-191	Sequence 191, Appl	621	3	50.0	37	1	US-08-682-485A-17	Sequence 17, Appl
549	3	50.0	26	4	US-08-467-344A-191	Sequence 191, Appl	622	3	50.0	37	1	US-08-682-485A-18	Sequence 18, Appl
550	3	50.0	27	2	US-08-967-999-8	Sequence 8, Appl	623	3	50.0	37	2	US-08-313-185-2	Sequence 2, Appl
551	3	50.0	27	2	US-08-967-999-9	Sequence 9, Appl	624	3	50.0	37	2	US-08-313-185-3	Sequence 3, Appl
552	3	50.0	27	3	US-08-256-747C-46	Sequence 46, Appl	625	3	50.0	37	2	US-08-459-499-5	Sequence 5, Appl
553	3	50.0	27	3	US-08-834-130A-46	Sequence 46, Appl	626	3	50.0	37	2	US-08-459-499-6	Sequence 6, Appl
554	3	50.0	28	1	US-08-402-282-5	Sequence 5, Appl	627	3	50.0	37	2	US-08-933-314-14	Sequence 14, Appl
555	3	50.0	28	1	US-08-508-004-5	Sequence 5, Appl	628	3	50.0	37	2	US-08-933-314-16	Sequence 16, Appl
556	3	50.0	28	1	US-08-402-066-5	Sequence 5, Appl	629	3	50.0	37	2	US-08-933-314-17	Sequence 17, Appl
557	3	50.0	28	1	US-08-402-068-5	Sequence 5, Appl	630	3	50.0	37	2	US-08-933-314-18	Sequence 18, Appl
558	3	50.0	28	4	US-09-407-687-38	Sequence 38, Appl	631	3	50.0	37	3	US-09-082-614A-2	Sequence 2, Appl
559	3	50.0	28	4	US-09-528-200-73	Sequence 73, Appl	632	3	50.0	37	3	US-09-082-614A-3	Sequence 3, Appl
560	3	50.0	29	3	US-08-895-474-11	Sequence 11, Appl	633	3	50.0	37	4	US-09-461-325-242	Sequence 242, App
561	3	50.0	29	4	US-09-058-740-3	Sequence 3, Appl	634	3	50.0	37	4	US-09-461-325-429	Sequence 429, App
562	3	50.0	29	4	US-09-205-258-630	Sequence 630, Appl	635	3	50.0	37	4	US-10-012-542-242	Sequence 242, App
563	3	50.0	29	4	US-09-690-454-161	Sequence 161, Appl	636	3	50.0	37	4	US-10-012-542-429	Sequence 429, App
564	3	50.0	30	1	US-08-117-083-25	Sequence 25, Appl	637	3	50.0	37	5	PCT-US93-08528-212	Patent No. 5177308
565	3	50.0	31	1	US-08-055-917-1	Sequence 1, Appl	638	3	50.0	37	6	5177308-12	Sequence 7, Appl
566	3	50.0	31	1	US-07-614-443A-6	Sequence 6, Appl	639	3	50.0	38	1	US-08-117-080-7	Sequence 8, Appl
567	3	50.0	31	1	US-08-095-068-1	Sequence 1, Appl	640	3	50.0	38	1	US-08-117-080-8	Sequence 8, Appl
568	3	50.0	31	1	US-07-934-656A-15	Sequence 15, Appl	641	3	50.0	38	1	US-08-176-500-134	Sequence 134, App
569	3	50.0	31	1	US-08-294-859-6	Sequence 6, Appl	642	3	50.0	38	1	US-08-118-270-210	Sequence 210, App
570	3	50.0	31	1	US-08-481-676-6	Sequence 6, Appl	643	3	50.0	38	1	US-08-118-270-211	Sequence 211, App
571	3	50.0	31	2	US-07-785-565A-1	Sequence 1, Appl	644	3	50.0	38	1	US-08-118-270-213	Sequence 213, App
572	3	50.0	32	1	US-08-140-721A-1	Sequence 1, Appl	645	3	50.0	38	1	US-08-471-052A-134	Sequence 134, App
573	3	50.0	32	1	US-08-619-790C-1	Sequence 1, Appl	646	3	50.0	38	1	US-08-471-329-7	Sequence 7, Appl
574	3	50.0	32	3	US-08-053-137A-68	Sequence 68, Appl	647	3	50.0	38	1	US-08-471-329-8	Sequence 8, Appl
575	3	50.0	32	4	US-09-085-761A-73	Sequence 73, Appl	648	3	50.0	38	1	US-08-189-331-134	Sequence 134, App
576	3	50.0	32	4	US-09-625-972-27	Sequence 27, Appl	649	3	50.0	38	1	US-08-682-485A-15	Sequence 15, Appl
577	3	50.0	32	4	US-09-308-345A-36	Sequence 36, Appl	650	3	50.0	38	1	US-08-682-485A-20	Sequence 20, Appl
578	3	50.0	32	4	US-09-308-345A-37	Sequence 37, Appl	651	3	50.0	38	2	US-08-471-939-134	Sequence 134, App
579	3	50.0	32	4	US-09-308-345A-39	Sequence 39, Appl	652	3	50.0	38	2	US-08-471-800-134	Sequence 134, App
580	3	50.0	32	4	US-08-308-345A-40	Sequence 40, Appl	653	3	50.0	38	2	US-08-915-142-7	Sequence 7, Appl
581	3	50.0	32	4	US-09-308-345A-41	Sequence 41, Appl	654	3	50.0	38	2	US-08-915-142-8	Sequence 8, Appl
582	3	50.0	33	1	US-08-290-448A-5	Sequence 5, Appl	655	3	50.0	38	2	US-08-471-068-134	Sequence 134, App
583	3	50.0	33	1	US-08-290-448A-6	Sequence 6, Appl	656	3	50.0	38	2	US-08-933-314-15	Sequence 15, Appl
584	3	50.0	33	1	US-08-290-448A-5	Sequence 5, Appl	657	3	50.0	38	2	US-08-933-314-20	Sequence 20, Appl
585	3	50.0	33	1	US-08-290-448A-6	Sequence 6, Appl	658	3	50.0	38	3	US-08-948-378A-6	Sequence 6, Appl
586	3	50.0	33	1	US-08-179-069A-5	Sequence 5, Appl	659	3	50.0	38	3	US-08-348-518C-21	Sequence 21, Appl
587	3	50.0	33	1	US-08-179-069A-6	Sequence 6, Appl	660	3	50.0	38	3	US-08-476-509B-21	Sequence 21, Appl
588	3	50.0	33	3	US-09-082-279B-1213	Sequence 1213, Ap	661	3	50.0	38	4	US-09-169-425C-6	Sequence 6, Appl
589	3	50.0	33	4	US-08-461-939B-5	Sequence 5, Appl	662	3	50.0	38	4	US-09-759-960-6	Sequence 6, Appl
590	3	50.0	33	4	US-08-461-939B-6	Sequence 6, Appl	663	3	50.0	38	4	US-09-646-691B-70	Sequence 70, Appl
591	3	50.0	33	4	US-08-464-000-5	Sequence 5, Appl	664	3	50.0	38	5	PCT-US93-08528-210	Sequence 210, App
592	3	50.0	33	4	US-08-464-000-6	Sequence 6, Appl	665	3	50.0	38	5	PCT-US93-08528-211	Sequence 211, App
593	3	50.0	33	4	US-09-315-304B-1213	Sequence 1213, Ap	666	3	50.0	38	5	PCT-US93-08528-213	Sequence 213, App
594	3	50.0	33	4	US-09-834-784-1213	Sequence 1213, Ap	667	3	50.0	38	6	5177308-8	Patent No. 5177308
595	3	50.0	33	4	US-09-515-965A-1213	Sequence 1213, Ap	668	3	50.0	39	5	PCT-US93-08528-214	Sequence 214, App
596	3	50.0	33	4	US-09-350-641C-1213	Sequence 1213, Ap	669	3	50.0	39	5	PCT-US93-08528-215	Sequence 215, App
597	3	50.0	35	1	US-08-190-802A-255	Sequence 255, App	670	3	50.0	40	3	US-08-803-346-65	Sequence 65, Appl
598	3	50.0	35	3	US-08-473-089-255	Sequence 255, App	671	3	50.0	40	3	US-08-988-856B-13	Sequence 13, Appl
600	3	50.0	35	4	US-08-473-089-255	Sequence 255, App	672	3	50.0	40	4	US-08-469-260A-541	Sequence 541, App
601	3	50.0	36	1	US-08-303-651-1	Sequence 1, Appl	673	3	50.0	40	4	US-08-475-399A-275	Sequence 275, App
602	3	50.0	36	3	US-09-082-279B-1051	Sequence 1051, Ap	674	3	50.0	40	4	US-08-488-446-541	Sequence 541, App
603	3	50.0	36	3	US-09-082-279B-1212	Sequence 1212, Ap	675	3	50.0	40	4	US-08-467-344A-541	Sequence 541, App
604	3	50.0	36	4	US-09-315-304B-1051	Sequence 1051, Ap	676	3	50.0	40	4	US-09-843-845-13	Sequence 13, Appl
605	3	50.0	36	4	US-09-315-304B-1212	Sequence 1212, Ap	677	3	50.0	40	5	PCT-US95-04910-10	Patent No. 5196194
606	3	50.0	36	4	US-09-276-600-7	Sequence 7, Appl	678	3	50.0	40	6	5196194-8	Sequence 793, App
607	3	50.0	36	4	US-09-834-784-1051	Sequence 1051, Ap	679	3	50.0	41	2	US-08-117-952-793	Sequence 793, App
608	3	50.0	36	4	US-09-834-784-1212	Sequence 1212, Ap	680	3	50.0	41	3	US-09-172-841-17	Sequence 17, Appl
609	3	50.0	36	4	US-09-779-451-53	Sequence 53, Appl	681	3	50.0	41	4	US-09-227-357-618	Sequence 618, App
610	3	50.0	36	4	US-09-779-451-71	Sequence 71, Appl	682	3	50.0	41	4	US-08-951-621-17	Sequence 17, Appl
611	3	50.0	36	4	US-09-515-965A-1051	Sequence 1051, Ap	683	3	50.0	41	6	5512648-1	Patent No. 5512648
							684	3	50.0	42	2	US-08-488-161-79	Sequence 79, Appl

685	3	50.0	42	3	US-09-273-685-79	Sequence 79, Appl	758	3	50.0	54	4	US-09-730-763-19	Sequence 19, Appl
686	3	50.0	42	3	US-08-894-699-66	Sequence 66, Appl	759	3	50.0	54	4	US-09-429-370-12	Sequence 12, Appl
687	3	50.0	42	3	US-09-444-410-66	Sequence 66, Appl	760	3	50.0	54	4	US-09-429-370-15	Sequence 15, Appl
688	3	50.0	42	4	US-09-205-258-1013	Sequence 1013, Ap	761	3	50.0	54	4	US-09-429-370-16	Sequence 16, Appl
689	3	50.0	42	5	PCT-US95-11934-79	Sequence 79, Appl	762	3	50.0	54	4	US-09-429-370-19	Sequence 19, Appl
690	3	50.0	42	3	US-08-488-161-77	Sequence 77, Appl	763	3	50.0	54	4	US-09-402-181B-302	Sequence 302, App
691	3	50.0	43	3	US-09-273-685-77	Sequence 77, Appl	764	3	50.0	54	4	US-09-721-456-302	Sequence 302, App
692	3	50.0	43	3	US-08-988-856B-5	Sequence 5, Appli	765	3	50.0	54	4	US-09-621-976-4731	Sequence 4731, Ap
693	3	50.0	43	3	US-08-843-845-5	Sequence 5, Appli	766	3	50.0	55	1	US-08-366-953A-36	Sequence 36, Appl
694	3	50.0	43	5	PCT-US95-11934-77	Sequence 77, Appl	767	3	50.0	55	1	US-08-366-953A-37	Sequence 37, Appl
695	3	50.0	44	3	US-08-894-483-5	Sequence 5, Appli	768	3	50.0	55	1	US-08-366-953A-38	Sequence 38, Appl
696	3	50.0	46	4	US-09-779-451-51	Sequence 51, Appl	769	3	50.0	55	1	US-08-366-953A-39	Sequence 39, Appl
697	3	50.0	46	4	US-09-779-451-59	Sequence 69, Appl	770	3	50.0	55	1	US-08-366-953A-42	Sequence 42, Appl
698	3	50.0	48	1	US-08-290-448A-7	Sequence 4, Appli	771	3	50.0	55	1	US-08-366-953A-43	Sequence 43, Appl
699	3	50.0	48	1	US-08-290-448A-7	Sequence 7, Appli	772	3	50.0	55	1	US-08-366-953A-44	Sequence 44, Appl
700	3	50.0	48	1	US-08-290-448A-4	Sequence 4, Appli	773	3	50.0	55	4	US-09-621-976-4235	Sequence 4235, Ap
701	3	50.0	48	1	US-08-290-448A-7	Sequence 7, Appli	774	3	50.0	55	4	US-09-621-976-6267	Sequence 6267, Ap
702	3	50.0	48	1	US-08-175-069A-4	Sequence 4, Appli	775	3	50.0	55	4	US-09-621-976-7689	Sequence 7689, Ap
703	3	50.0	48	1	US-08-175-069A-7	Sequence 7, Appli	776	3	50.0	56	2	US-08-557-309B-28	Sequence 28, Appl
704	3	50.0	48	2	US-08-637-759B-199	Sequence 199, App	777	3	50.0	56	2	US-08-850-910A-24	Sequence 24, Appl
705	3	50.0	48	3	US-08-871-355A-199	Sequence 199, App	778	3	50.0	56	3	US-08-834-306-28	Sequence 28, Appl
706	3	50.0	48	4	US-08-461-939B-4	Sequence 4, Appli	779	3	50.0	56	3	US-08-993-674A-28	Sequence 28, Appl
707	3	50.0	48	4	US-08-461-939B-7	Sequence 7, Appli	780	3	50.0	56	4	US-09-227-357-671	Sequence 671, App
708	3	50.0	48	4	US-08-464-000-4	Sequence 4, Appli	781	3	50.0	56	4	US-08-894-626-4	Sequence 4, Appli
709	3	50.0	48	4	US-08-464-000-7	Sequence 7, Appli	782	3	50.0	56	4	US-09-256-976-28	Sequence 28, Appl
710	3	50.0	48	4	US-09-201-945-199	Sequence 199, App	783	3	50.0	56	4	US-09-205-258-359	Sequence 359, App
711	3	50.0	48	4	US-09-227-357-241	Sequence 241, App	784	3	50.0	56	4	US-09-621-976-6726	Sequence 6726, Ap
712	3	50.0	49	1	US-08-387-156-4	Sequence 4, Appli	785	3	50.0	57	4	US-09-621-976-6039	Sequence 6039, Ap
713	3	50.0	49	2	US-08-694-865-4	Sequence 4, Appli	786	3	50.0	57	4	US-09-621-976-6935	Sequence 6935, Ap
714	3	50.0	49	2	US-08-878-748-4	Sequence 4, Appli	787	3	50.0	58	2	US-08-408-095-34	Sequence 34, Appl
715	3	50.0	49	3	US-09-124-491-4	Sequence 4, Appli	788	3	50.0	58	3	US-09-369-494-1	Sequence 1, Appli
716	3	50.0	49	4	US-08-475-399A-276	Sequence 276, App	789	3	50.0	58	3	US-08-965-762-11	Sequence 11, Appl
717	3	50.0	49	4	US-09-383-912-4	Sequence 4, Appli	790	3	50.0	58	4	US-09-227-357-240	Sequence 240, App
718	3	50.0	49	4	US-09-148-545-245	Sequence 245, App	791	3	50.0	59	1	US-08-358-160-118	Sequence 118, App
719	3	50.0	50	1	US-07-614-443A-5	Sequence 5, Appli	792	3	50.0	59	3	US-08-513-974B-25	Sequence 25, Appl
720	3	50.0	50	1	US-08-294-859-5	Sequence 5, Appli	793	3	50.0	59	3	US-08-776-971-20	Sequence 20, Appl
721	3	50.0	50	1	US-08-481-676-5	Sequence 5, Appli	794	3	50.0	59	4	US-09-911-927-11	Sequence 11, Appl
722	3	50.0	50	3	US-09-053-197A-67	Sequence 67, Appl	795	3	50.0	59	4	US-09-911-882-11	Sequence 11, Appl
723	3	50.0	50	3	US-09-177-249-94	Sequence 94, Appl	796	3	50.0	59	4	US-09-638-715-33	Sequence 33, Appl
724	3	50.0	51	2	US-09-085-761A-72	Sequence 72, Appl	797	3	50.0	59	4	US-09-911-888-11	Sequence 11, Appl
725	3	50.0	51	2	US-08-464-517-13	Sequence 13, Appl	798	3	50.0	59	4	US-09-461-436B-25	Sequence 25, Appl
726	3	50.0	51	2	US-08-633-879C-10	Sequence 10, Appl	799	3	50.0	59	4	US-10-060-509-33	Sequence 33, Appl
727	3	50.0	51	2	US-08-246-361A-13	Sequence 13, Appl	800	3	50.0	59	4	US-09-621-976-4644	Sequence 4644, Ap
728	3	50.0	51	4	US-08-463-772-13	Sequence 13, Appl	801	3	50.0	59	4	US-09-621-976-5501	Sequence 5501, Ap
729	3	50.0	51	3	US-09-369-494-9	Sequence 9, Appli	802	3	50.0	59	4	US-10-060-506-33	Sequence 33, Appl
730	3	50.0	51	4	US-09-621-976-4432	Sequence 4432, Ap	803	3	50.0	59	6	5466783-13	Patent No. 5466783
731	3	50.0	51	4	US-09-621-976-4433	Sequence 4433, Ap	804	3	50.0	60	2	US-08-484-397A-28	Sequence 28, Appl
732	3	50.0	51	4	US-08-621-976-7188	Sequence 7188, Ap	805	3	50.0	60	2	US-08-484-397A-29	Sequence 29, Appl
733	3	50.0	51	4	US-08-621-976-7656	Sequence 7656, Ap	806	3	50.0	60	2	US-08-484-397A-30	Sequence 30, Appl
734	3	50.0	51	4	US-09-621-976-7660	Sequence 7660, Ap	807	3	50.0	60	2	US-08-484-397A-31	Sequence 31, Appl
735	3	50.0	51	5	PCT-US93-05000-13	Sequence 13, Appl	808	3	50.0	60	2	US-08-484-397A-34	Sequence 34, Appl
736	3	50.0	51	6	5274075-11	Patent No. 5274075	809	3	50.0	60	2	US-08-484-397A-35	Sequence 35, Appl
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738	3	50.0	52	3	US-08-369-494-17	Sequence 17, Appl	811	3	50.0	60	2	US-08-484-397A-37	Sequence 37, Appl
739	3	50.0	52	3	US-09-358-569D-15	Sequence 15, Appl	812	3	50.0	60	4	US-09-638-715-20	Sequence 20, Appl
740	3	50.0	52	4	US-09-621-976-5773	Sequence 5773, Ap	813	3	50.0	60	4	US-09-638-715-21	Sequence 21, Appl
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742	3	50.0	54	3	US-08-917-299-12	Sequence 12, Appl	815	3	50.0	60	4	US-10-060-509-20	Sequence 20, Appl
743	3	50.0	54	3	US-08-917-299-15	Sequence 15, Appl	816	3	50.0	60	4	US-10-060-509-21	Sequence 21, Appl
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746	3	50.0	54	3	US-08-851-843A-183	Sequence 183, App	819	3	50.0	60	4	US-09-489-039A-8043	Sequence 8043, Ap
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753	3	50.0	54	4	US-09-430-323-183	Sequence 183, App	826	3	50.0	61	4	US-09-205-258-478	Sequence 478, App
754	3	50.0	54	4	US-09-205-258-767	Sequence 767, App	827	3	50.0	61	4	US-09-107-532A-5825	Sequence 5825, Ap
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831	3	50.0	62	4	US-09-252-991A-28943	Sequence 28943, A	904	73	4	US-09-134-000C-4681	Sequence 4681, Ap
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833	3	50.0	62	4	US-09-252-991A-23832	Sequence 23832, A	906	74	1	US-08-379-538-3	Sequence 3, Appli
834	3	50.0	63	4	US-08-311-731A-311	Sequence 311, Appl	907	74	1	US-08-379-538-4	Sequence 4, Appli
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837	3	50.0	64	4	US-09-632-287A-15	Sequence 15, Appl	910	74	4	US-09-252-991A-26626	Sequence 26626, A
838	3	50.0	64	4	US-09-134-000C-6722	Sequence 6722, Ap	911	74	4	US-09-252-991A-30664	Sequence 30664, A
839	3	50.0	64	4	US-09-673-395A-244	Sequence 244, App	912	74	4	US-09-489-039A-12609	Sequence 12609, A
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853	3	50.0	67	4	US-09-621-976-7215	Sequence 7215, Ap	926	76	4	US-09-621-976-5645	Sequence 5645, Ap
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860	3	50.0	68	4	US-09-540-236-1990	Sequence 1990, Ap	933	77	4	US-09-673-395A-288	Sequence 288, App
861	3	50.0	69	2	US-08-245-511-31	Sequence 31, Appl	934	77	4	US-09-621-976-4163	Sequence 4163, Ap
862	3	50.0	69	2	US-08-245-511-32	Sequence 32, Appl	935	77	4	US-09-621-976-5520	Sequence 5520, Ap
863	3	50.0	69	2	US-08-600-993A-31	Sequence 31, Appl	936	78	2	US-08-612-788-22	Sequence 22, Appl
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868	3	50.0	69	4	US-09-489-039A-11833	Sequence 11833, A	941	78	4	US-08-488-446-234	Sequence 234, App
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872	3	50.0	70	3	US-08-905-223-469	Sequence 469, App	945	79	4	US-09-149-476-378	Sequence 378, App
873	3	50.0	70	4	US-09-134-001C-5312	Sequence 5312, Ap	946	79	4	US-09-145-236B-95	Sequence 95, Appl
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875	3	50.0	70	4	US-09-148-545-143	Sequence 143, App	948	79	4	US-08-311-731A-270	Sequence 270, App
876	3	50.0	70	4	US-09-673-395A-281	Sequence 281, App	949	79	4	US-09-107-532A-5914	Sequence 5914, Ap
877	3	50.0	70	4	US-09-621-976-5707	Sequence 5707, Ap	950	79	4	US-09-540-236-3183	Sequence 3183, Ap
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880	3	50.0	71	1	US-08-055-917-17	Sequence 17, Appl	953	80	4	US-08-311-731A-344	Sequence 344, App
881	3	50.0	71	1	US-08-095-068-15	Sequence 15, Appl	954	80	4	US-09-543-681A-7619	Sequence 7619, Ap
882	3	50.0	71	1	US-08-095-068-17	Sequence 17, Appl	955	81	4	US-08-858-207A-336	Sequence 336, App
883	3	50.0	71	1	US-08-140-721A-15	Sequence 15, Appl	956	81	4	US-08-469-260A-187	Sequence 187, App
884	3	50.0	71	1	US-08-140-721A-17	Sequence 17, Appl	957	81	4	US-08-220-602B-25	Sequence 25, Appl
885	3	50.0	71	1	US-08-280-443-22	Sequence 22, Appl	958	81	4	US-08-488-446-187	Sequence 187, App
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894	3	50.0	71	4	US-09-621-976-6815	Sequence 6815, Ap	967	83	4	US-09-375-314-12	Sequence 12, Appl
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898	3	50.0	72	4	US-09-621-976-4838	Sequence 4838, Ap	971	83	4	US-09-489-039A-7681	Sequence 7681, Ap
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Sequence 8463, Ap
Sequence 6241, Ap
Sequence 7155, Ap

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ALIGNMENTS

RESULT 1
US-09-252-991A-18367
; Sequence 18367, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18367
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18367

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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6
Db 2 DWSWA 6

RESULT 2
US-09-252-991A-31533
; Sequence 31533, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31533
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31533

Query Match 83.3%; Score 5; DB 4; Length 142;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 94 ADWSW 98

RESULT 3
US-09-325-932A-163
; Sequence 163, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 163
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-163

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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 109 ADWSW 113

RESULT 4
US-09-325-932A-162
; Sequence 162, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 162
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-162

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Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5
Db 109 ADWSW 113

Db 100 ADWSW 104

RESULT 5
US-09-632-570-17
; Sequence 17, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949a1 Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632.570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-570-17

Query Match 83.3%; Score 5; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 63 ADWSW 67

RESULT 6
US-09-632-575-47
; Sequence 47, Application US/09632575
; Patent No. 6635465
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Ropp, Traci M.
; TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
; TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
; FILE REFERENCE: GC629
; CURRENT APPLICATION NUMBER: US/09/632.575
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Gliocladium roseum (3)
US-09-632-575-47

Query Match 83.3%; Score 5; DB 4; Length 236;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 63 ADWSW 67

RESULT 7
US-09-345-236B-3
; Sequence 3, Application US/09345236B
; Patent No. 6521454
; GENERAL INFORMATION:
; APPLICANT: Becnel, James J.
; APPLICANT: Tukuo, Fukuda
; APPLICANT: Moser, Bettina
; APPLICANT: Cockburn, Andrew
; APPLICANT: White, Susan E.

; APPLICANT: Undeen, Albert H.
; TITLE OF INVENTION: No. 6521454e1 Baculoviruses, Insecticidal
; TITLE OF INVENTION: Compositions, and Methods for Control of Invertebrates
; FILE REFERENCE: 21042.0004
; CURRENT APPLICATION NUMBER: US/09/345.236B
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 242
; TYPE: PRT
; ORGANISM: mosquito baculovirus
US-09-345-236B-3

Query Match 83.3%; Score 5; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 80 DWSWA 84

RESULT 8
US-09-325-932A-158
; Sequence 158, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325.932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 158
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-09-325-932A-158

Query Match 83.3%; Score 5; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 128 ADWSW 132

RESULT 9
US-09-252-991A-22368
; Sequence 22368, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22368
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22368

```
Query Match      83.3%; Score 5; DB 4; Length 445;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      304 DWSWA 308

RESULT 10
US-09-252-991A-21704
; Sequence 21704, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21704
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21704

Query Match      83.3%; Score 5; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSWA 6
      |||||
Db      169 DWSWA 173

RESULT 11
5217869-75
; Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 75
; LENGTH: 5
5217869-75

Query Match      66.7%; Score 4; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DWSW 5
      |||||
Db      1 DWSW 4

RESULT 12
US-08-435-925C-9
; Sequence 9, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCYTTALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
; ADDRESSEE: No. 5646025o No. 5646025disk of No. 5646025th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,925C
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4429.000-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-435-925C-9

Query Match      66.7%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db      1 ADWS 4

RESULT 13
US-08-435-925C-10
; Sequence 10, Application US/08435925C
; Patent No. 5646025
; GENERAL INFORMATION:
; APPLICANT: Moyer, Donna
; TITLE OF INVENTION: SCYTTALIDUM CATALASE GENE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5646025o No. 5646025disk of No. 5646025th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/435,925C
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4429.000-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
```

```
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-435-925C-10

Query Match 66.7%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 1 ADWS 4

RESULT 14
US-08-190-788A-246
; Sequence 246, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 312
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies N.V.
; STREET: 4001 Miranda Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,788A
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,567
; FILING DATE: 05-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.1
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-190-788A-246

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 7 ADWS 10

RESULT 15
US-08-383-474B-249
; Sequence 249, Application US/08383474B
```

```
; Patent No. 5767234
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.
; APPLICANT: Jacobs, Jeff W.
; TITLE OF INVENTION: Peptides and Compounds That Bind to
; TITLE OF INVENTION: the IL-1 Receptor
; NUMBER OF SEQUENCES: 314
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend & Townsend & Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/383,474B
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 1019.3
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-383-474B-249

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 7 ADWS 10

RESULT 16
US-08-465-391A-246
; Sequence 246, Application US/08465391A
; Patent No. 5786331
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
```

```
;
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331v1el, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-465-391A-246

Query Match 66.7%; Score 4; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 7 ADWS 10

RESULT 17
US-08-464-538B-246
; Sequence 246, Application US/08464538B
; Patent No. 5861476
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Philippe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/464,538B
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 16528A-001810
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-464-538B-246

Query Match 66.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWS 4
Db 7 ADWS 10

RESULT 18
US-08-463-076E-303
; Sequence 303, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 303:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
```

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-303

Query Match          66.7%; Score 4; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 7 ADWS 10

RESULT 19
US-09-428-082B-866
; Sequence 866, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428.082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 866
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-09-428-082B-866

Query Match          66.7%; Score 4; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
Db 7 ADWS 10

RESULT 20
US-08-905-223-274
; Sequence 274, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905.223
; FILING DATE:
```

```
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 274:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -26..-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 9.6
; OTHER INFORMATION: seq WLIALASWSWALC/RI
US-08-905-223-274

Query Match          66.7%; Score 4; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 21 WSWA 24

RESULT 21
US-08-379-538-2
; Sequence 2, Application US/08379538
; Patent No. 5804554
; GENERAL INFORMATION:
; APPLICANT: Volkman, Robert A.
; APPLICANT: Saccomano, Nicholas A.
; APPLICANT: Nason II, Deane M.
; APPLICANT: Heck, Steven D.
; APPLICANT: Ronau, Robert T.
; TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc
; STREET: 235 East 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,538
; FILING DATE: 3-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/887073
; FILING DATE: 21-MAY-1992
; APPLICATION NUMBER: PCT/US93/03921
; FILING DATE: 30-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Zielinski, Bryan
; REGISTRATION NUMBER: 34,462
; REFERENCE/DOCKET NUMBER: PC8175A
; TELECOMMUNICATION INFORMATION:
```

```

; TELEPHONE: (212) 573-4585
; TELEFAX: (212) 573-1939
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 74 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: venom
US-08-379-538-2

Query Match          66.7%; Score 4; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DMSW 5
Db      52 DMSW 55

RESULT 22
US-09-177-249-184
; Sequence 184, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: Development in Plants
; CURRENT APPLICATION NUMBER: US/09/177,249
; EARLIER FILING DATE: 1998-10-22
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 184
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-184

Query Match          66.7%; Score 4; DB 3; Length 78;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      54 ADWS 57

RESULT 23
US-09-252-991A-27207
; Sequence 27207, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27207
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27207

Query Match          66.7%; Score 4; DB 4; Length 79;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      13 ADWS 16

RESULT 24
US-09-621-976-4160
; Sequence 4160, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4160
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -15...-1
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa = Asn,Ser
; NAME/KEY: UNSURE
; LOCATION: 58
; OTHER INFORMATION: Xaa = Lys,Thr
US-09-621-976-4160

Query Match          66.7%; Score 4; DB 4; Length 80;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
Db      39 WSWA 42

RESULT 25
US-09-251-372-4
; Sequence 4, Application US/09251372
; Patent No. 6238886
; GENERAL INFORMATION:
; APPLICANT: PATEL, LISA
; TITLE OF INVENTION: NOVEL COMPOUNDS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Preetia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482

```


COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,372
FILING DATE: 16-FEB-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9900823.7
FILING DATE: 14-JAN-1999
APPLICATION NUMBER: 9803290.7
FILING DATE: 16-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-30012A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-251-372-4

Query Match 66.7%; Score 4; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 72 WSWA 75

RESULT 26
US-09-811-241-4
Sequence 4, Application US/09811241
Patent No. 6348341
GENERAL INFORMATION:
APPLICANT: MACPHEE, COLIN HOUSTON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30012A-D1
CURRENT APPLICATION NUMBER: US/09/811,241
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/251,372
PRIOR FILING DATE: 1999-02-16
PRIOR APPLICATION NUMBER: 9900823.7
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 9803290.7
PRIOR FILING DATE: 1998-02-16
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 84
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-811-241-4

Query Match 66.7%; Score 4; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 72 WSWA 75

RESULT 27
US-09-252-991A-19040
Sequence 19040, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19040
LENGTH: 84
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19040

Query Match 66.7%; Score 4; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMS 4
Db 32 ADMS 35

RESULT 28
US-09-252-991A-31932
Sequence 31932, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31932
LENGTH: 95
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31932

Query Match 66.7%; Score 4; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WSWA 6
Db 91 WSWA 94

RESULT 29
US-08-241-853-28
Sequence 28, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
TITLE OF INVENTION: AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 37

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-241-853-28

Query Match 66.7%; Score 4; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 20 DWSW 23

RESULT 31
US-08-850-917-28
Sequence 28, Application US/08850917
Patent No. 5854045
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/850,917
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/241,853
FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-28

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-850-917-28

Query Match 66.7%; Score 4; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSW 5
Db 20 DWSW 23

RESULT 30
US-08-241-853-29
Sequence 29, Application US/08241853
Patent No. 5693488
GENERAL INFORMATION:
APPLICANT: Fang, Kathy S.
APPLICANT: Hanafusa, Hidesaburo
TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/241,853
FILING DATE: 12-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
```

Query Match 66.7%; Score 4; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWS 5
 ||||
 Db 20 DWS 23

RESULT 32

US-08-850-917-29
 ; Sequence 29, Application US/08850917
 ; Patent No. 5854045
 ; GENERAL INFORMATION:
 ; APPLICANT: Fang, Kathy S.
 ; APPLICANT: Hanafusa, Hidesaburo
 ; TITLE OF INVENTION: A TRANSMEMBRANE TYROSINE PHOSPHATASE
 ; TITLE OF INVENTION: AND METHODS OF USE THEREOF
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/850,917
 ; FILING DATE: 02-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/241,853
 ; FILING DATE: 12-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-078
 ; TELEPHONE: 201 487-5800
 ; TELEFAX: 201 343-1684
 ; TELEX: 133521

INFORMATION FOR SEQ ID NO: 29:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 100 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-850-917-29

Query Match 66.7%; Score 4; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWS 5
 ||||
 Db 20 DWS 23

RESULT 33

US-08-585-585A-4
 ; Sequence 4, Application US/08585585A
 ; Patent No. 5874308
 ; GENERAL INFORMATION:
 ; APPLICANT: Kilburn, Douglas G.
 ; APPLICANT: Humphries, Keith R.

APPLICANT: Doheny, James G.
 APPLICANT: Jervis, Eric
 APPLICANT: Allmonti, Judie
 TITLE OF INVENTION: Compositions and methods for modulating
 cell proliferation using growth factor-polysaccharide
 binding fusion proteins
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rae-Venter Law Group
 STREET: Box 60039
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94306

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/585,585A
 ; FILING DATE: 16-JAN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kung, Viola T.

REGISTRATION NUMBER: 41,131
 REFERENCE/DOCKET NUMBER: CBDT.016.000S
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)328-4400
 ; TELEFAX: (650)328-4477

INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 106 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; US-08-585-585A-4

Query Match 66.7%; Score 4; DB 2; Length 106;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWS 4
 ||||
 Db 52 ADWS 55

RESULT 34

US-08-249-037C-4
 ; Sequence 4, Application US/08249037C
 ; Patent No. 5928917
 ; GENERAL INFORMATION:

APPLICANT: Kilburn, Douglas G.
 APPLICANT: Miller, Robert C.
 APPLICANT: Warren, Richard A.J.
 APPLICANT: Gilkes, Neil R.

TITLE OF INVENTION: Polysaccharide binding fusion proteins
 and conjugates
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Rae-Venter Law Group, P.C.
 STREET: P.O.Box 60039
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94306

COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:

Query Match	66.7%	Score 4;	DB 2;	Length 106;
Best Local Similarity	100.0%;	Pred. No. 49;		
Matches	4;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

Query Match 66.7%; Score 4; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4: Conservative 0; Mismatches 0; Indels

Qy	1	ADWS	4
Dh	52	ADWS	55

RESULT 36
US-08-788-621B-4
; Sequence 4, Application US/08788621B
; Patent No. 6124117
; GENERAL INFORMATION:
; APPLICANT: Kilburn, Douglas G.
; APPLICANT: Miller, Robert C.
; APPLICANT: Warren, Richard A.J.
; APPLICANT: Gilkes, Neil R.
; TITLE OF INVENTION: Polysaccharide binding fusion proteins
; TITLE OF INVENTION: and conjugates
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: P.O.Box 60039
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,621B
; FILING DATE: January 23, 1997
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/249,037
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/865,095
; FILING DATE: 08-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/603,987
; FILING DATE: 25-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/216,794
; FILING DATE: 08-JUL-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Kung, Viola T.
; REGISTRATION NUMBER: 41,131
; REFERENCE/DOCKET NUMBER: CBPT.002.05US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)328-4400

RESULT 36

TELEFAX: (650)328-4477
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-788-621B-4

Query Match 66.7%; Score 4; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADWS 4
|
|
|
|
Db 52 ADWS 55

RESULT 37

US-08-477-270-20
; Sequence 20, Application US/08477270
; Patent No. 5629158
; GENERAL INFORMATION:
; APPLICANT: UHLEN, Mathias
; TITLE OF INVENTION: SOLID PHASE DIAGNOSIS OF MEDICAL
; TITLE OF INVENTION: CONDITIONS
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,270
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/261,010
; FILING DATE:
; APPLICATION NUMBER: US 07/781,157
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 15787/153 DFBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-270-20

Query Match 66.7%; Score 4; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADWS 4
|
|
|
|
Db 31 ADWS 34

RESULT 38
US-09-149-476-360
; Sequence 360, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11

EARLIER APPLICATION NUMBER: 60/043,568	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315	EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974	EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637	EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,888	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911	EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,910	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,761	EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595	EARLIER FILING DATE: 1997-08-22

QY 3 WSWA 6
 ||||
 Db 32 WSWA 35

RESULT 39
 US-09-673-395A-204
 ; Sequence 204, Application US/09673395A
 ; Patent No. 6620923
 ; GENERAL INFORMATION:
 ; APPLICANT: SPECHT, THOMAS

```
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKI, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673,395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 204
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-673-395A-204

Query Match      66.7%; Score 4; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 WSWA 6
      |||||
Db     102 WSWA 105

RESULT 40
US-09-543-681A-7177
; Sequence 7177, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7177
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7177

Query Match      66.7%; Score 4; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db     94 ADWS 97

RESULT 41
US-09-252-991A-20154
; Sequence 20154, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20154
; LENGTH: 138
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20154

Query Match      66.7%; Score 4; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db     45 ADWS 48

RESULT 42
US-09-257-583-13
; Sequence 13, Application US/09257583A
; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; CURRENT FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Zea mays
US-09-257-583-13

Query Match      66.7%; Score 4; DB 4; Length 163;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
      |||||
Db     87 ADWS 90

RESULT 43
US-09-252-991A-23817
; Sequence 23817, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23817
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23817

Query Match      66.7%; Score 4; DB 4; Length 164;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 WSWA 6
      |||||
Db     134 WSWA 137

RESULT 44
US-09-199-637A-339
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; Sequence 339, Application US/09199637A
; Patent No. 6355411
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick
; APPLICANT: Goodman, Howard M.
; APPLICANT: Rahme, Laurence G.
; APPLICANT: Mahajan-Miklos, Shalina
; APPLICANT: Tan, Man-Wah
; APPLICANT: Cao, Hui
; APPLICANT: Drenkard, Eliana
; APPLICANT: Tsongalis, John
; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361002
; CURRENT APPLICATION NUMBER: US/09/199,637A
; CURRENT FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-339

Query Match          66.7%; Score 4; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 DWSW 5
Db      31 DWSW 34

RESULT 45
US-09-252-991A-23876
; Sequence 23876, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23876
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23876

Query Match          66.7%; Score 4; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      56 ADWS 59

RESULT 46
US-09-252-991A-17160
; Sequence 17160, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17160
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17160

Query Match          66.7%; Score 4; DB 4; Length 189;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 WSWA 6
Db      61 WSWA 64

RESULT 47
US-09-252-991A-28753
; Sequence 28753, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28753
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28753

Query Match          66.7%; Score 4; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ADWS 4
Db      158 ADWS 161

RESULT 48
US-09-134-000C-3705
; Sequence 3705, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3705
; LENGTH: 191
; TYPE: PRT
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3705

Query Match      66.7%; Score 4; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
Db      162 ADWS 165

RESULT 49
US-09-489-039A-12525
; Sequence 12525, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12525
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12525

Query Match      66.7%; Score 4; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
Db      147 ADWS 150

RESULT 50
US-09-540-236-2208
; Sequence 2208, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2208
; LENGTH: 201
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2208

Query Match      66.7%; Score 4; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ADWS 4
Db      120 ADWS 123

Search completed: July 23, 2004, 13:28:17
Job time : 28 secs
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OM protein - protein search, using sw model

Run on: July 23, 2004, 13:20:30 ; Search time 52 Seconds
(without alignments)
32.602 Million cell updates/sec

Title: US-09-847-940C-6
Perfect score: 6
Sequence: 1 ADWSWA 6

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

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Minimum DB seq length: 0

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7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	6	100.0	6	5	AAm48538 Anti-infl
2	6	100.0	6	5	AAm48570 Anti-infl
3	6	100.0	6	6	ADA61814 NFKB esse
4	6	100.0	6	6	ADA61846 NFKB esse
5	6	100.0	7	5	AAm48574 Anti-infl
6	6	100.0	7	6	ADA61850 NFKB esse
7	6	100.0	8	5	AAm48575 Anti-infl
8	6	100.0	8	5	AAm48567 Anti-infl
9	6	100.0	8	6	ADA61851 NFKB esse
10	6	100.0	8	6	ADA61843 NFKB esse
11	6	100.0	9	5	AAm48573 Anti-infl
12	6	100.0	9	5	AAm48566 Anti-infl
13	6	100.0	9	5	AAm48569 Anti-infl
14	6	100.0	9	5	AAm48572 Anti-infl
15	6	100.0	9	6	ADA61848 NFKB esse
16	6	100.0	9	6	ADA61841 NFKB esse
17	6	100.0	9	6	ADA61849 NFKB esse
18	6	100.0	9	6	ADA61845 NFKB esse
19	6	100.0	9	6	ADA61842 NFKB esse
20	6	100.0	10	5	AAm48568 Anti-infl
21	6	100.0	10	5	AAm48571 Anti-infl
22	6	100.0	10	6	ADA61844 NFKB esse
23	6	100.0	10	6	ADA61847 NFKB esse
24	6	100.0	11	5	AAm48565 Anti-infl
25	6	100.0	11	6	ADA61840 NFKB esse

26	5	83.3	6	5	ABB08727 Mutated I
27	5	83.3	6	5	ABB08728 Mutated I
28	5	83.3	6	5	AAm48537 Anti-infl
29	5	83.3	6	5	AAm48548 Anti-infl
30	5	83.3	6	5	AAm48559 Anti-infl
31	5	83.3	6	5	AAm48509 NBD mutan
32	5	83.3	6	5	AAm48510 NBD mutan
33	5	83.3	6	5	AAm48536 Anti-infl
34	5	83.3	6	6	ABU08420 Human NEM
35	5	83.3	6	6	ABU08421 Human NEM
36	5	83.3	6	6	ADA61778 IKKbeta N
37	5	83.3	6	6	ADA61812 NFKB esse
38	5	83.3	6	6	ADA61811 NFKB esse
39	5	83.3	6	6	ADA61813 NFKB esse
40	5	83.3	6	6	ADA61835 NFKB esse
41	5	83.3	6	6	ADA61779 IKKbeta N
42	5	83.3	6	6	ADA61824 NFKB esse
43	5	83.3	7	5	AAm48552 Anti-infl
44	5	83.3	7	5	AAm48563 Anti-infl
45	5	83.3	7	6	ADA61828 NFKB esse
46	5	83.3	7	6	ADA61839 NFKB esse
47	5	83.3	8	5	AAm48556 Anti-infl
48	5	83.3	8	5	AAm48545 Anti-infl
49	5	83.3	8	5	AAm48564 Anti-infl
50	5	83.3	8	5	AAm48553 Anti-infl
51	5	83.3	8	6	ADA61829 NFKB esse
52	5	83.3	8	6	ADA61821 NFKB esse
53	5	83.3	9	5	AAm48562 Anti-infl
54	5	83.3	9	5	AAm48561 Anti-infl
55	5	83.3	9	5	AAm48558 Anti-infl
56	5	83.3	9	5	AAm48555 Anti-infl
57	5	83.3	9	5	AAm48551 Anti-infl
58	5	83.3	9	5	AAm48547 Anti-infl
59	5	83.3	9	5	AAm48550 Anti-infl
60	5	83.3	9	6	ADA61823 NFKB esse
61	5	83.3	9	6	ADA61827 NFKB esse
62	5	83.3	9	6	ADA61826 NFKB esse
63	5	83.3	9	6	ADA61831 NFKB esse
64	5	83.3	9	6	ADA61833 NFKB esse
65	5	83.3	9	6	ADA61834 NFKB esse
66	5	83.3	9	6	ADA61837 NFKB esse
67	5	83.3	9	6	ADA61838 NFKB esse
68	5	83.3	9	6	ADA61820 NFKB esse
69	5	83.3	10	5	AAm48546 Anti-infl
70	5	83.3	10	5	AAm48557 Anti-infl
71	5	83.3	10	5	AAm48560 Anti-infl
72	5	83.3	10	5	AAm48549 Anti-infl
73	5	83.3	10	5	AAm48554 Anti-infl
74	5	83.3	10	6	ADA61836 NFKB esse
75	5	83.3	10	6	ADA61825 NFKB esse
76	5	83.3	10	6	ADA61822 NFKB esse
77	5	83.3	10	6	ADA61832 NFKB esse
78	5	83.3	10	6	ADA61830 NFKB esse
79	5	83.3	11	5	AAm48543 Anti-infl
80	5	83.3	11	6	ADA61819 NFKB esse
81	5	83.3	31	5	AAU90785 Insulin/1
82	5	83.3	50	4	AAm85714 Human imm
83	5	83.3	103	2	AAU06332 Gliocla
84	5	83.3	174	4	AAm85780 Cysteine
85	5	83.3	174	7	ADB94799 Programme
86	5	83.3	218	2	AAW30839 MyoKL pro
87	5	83.3	225	4	AAm85779 Cysteine
88	5	83.3	225	7	ADB94798 Programme
89	5	83.3	236	2	AAU06363 Gliocla
90	5	83.3	236	3	AAU84341 Amino aci
91	5	83.3	236	3	AAU84341 Amino aci
92	5	83.3	236	5	AAU77584 Gliocla
93	5	83.3	236	5	AAU77584 G. roscum
94	5	83.3	242	7	ABO22372 Mosquito
95	5	83.3	274	5	ABP65718 Bifidobac
96	5	83.3	276	4	AAm39444 Human pol
97	5	83.3	277	3	AAm42053 Human ORF
98	5	83.3	277	3	AAm42053 Human ORF

99	5	83.3	277	7	ADB94916	Adb94916 Programme	172	4	66.7	17	6	ADA61932	Ada61932 NFkB esse
100	5	83.3	289	4	ABG24678	Abg24678 Novel hum	173	4	66.7	17	6	ADA61915	Ada61915 NFkB esse
101	5	83.3	371	4	Am41230	Am41230 Human pol	174	4	66.7	17	6	ADA61914	Ada61914 NFkB esse
102	5	83.3	378	4	Ab65775	Ab65775 Cysteine	175	4	66.7	17	6	ADA61919	Ada61919 NFkB esse
103	5	83.3	378	7	ADB94794	Adb94794 Programme	176	4	66.7	17	6	ADA61920	Ada61920 NFkB esse
104	5	83.3	452	4	Am93545	Am93545 Human pol	177	4	66.7	17	6	ADA61931	Ada61931 NFkB esse
105	5	83.3	501	6	ABR92162	AbR92162 Human cer	178	4	66.7	18	5	AAm48628	Aam48628 Anti-infl
106	5	83.3	452	4	ABB62635	Abb62635 Drosophil	179	4	66.7	18	5	AAm48632	Aam48632 Anti-infl
107	5	83.3	597	4	ABB77291	Abb77291 Human IKK	180	4	66.7	18	5	AAm48633	Aam48633 Anti-infl
108	5	83.3	745	5	ABB77292	Abb77292 Human IKK	181	4	66.7	18	5	AAm48629	Aam48629 Anti-infl
109	5	83.3	756	5	ABB77308	Abb77308 Human IKK	182	4	66.7	18	5	AAm48634	Aam48634 Anti-infl
110	5	83.3	756	5	ABB77309	Abb77309 Human IKK	183	4	66.7	18	5	AAm48635	Aam48635 Anti-infl
111	5	83.3	1005	5	ABB93598	Abb93598 Herbicida	184	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
112	5	83.3	5435	4	AAE10145	Aae10145 Streptomy	185	4	66.7	18	6	ADA61905	Ada61905 NFkB esse
113	4	66.7	5	2	AAR12717	Aar12717 Pentapept	186	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
114	4	66.7	5	2	AAR15181	Aar15181 Mimotope	187	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
115	4	66.7	5	2	AAR69949	Aar69949 Pentameri	188	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
116	4	66.7	5	2	AAR69895	Aar69895 Peptide 7	189	4	66.7	18	6	ADA61904	Ada61904 NFkB esse
117	4	66.7	6	5	ABB08725	Abb08725 IKKbeta N	190	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
118	4	66.7	6	5	AAm48655	Aam48655 NBD mutan	191	4	66.7	18	6	ADA61905	Ada61905 NFkB esse
119	4	66.7	6	5	AAm48530	Aam48530 Anti-infl	192	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
120	4	66.7	6	6	ABU08418	Abu08418 Human NEM	193	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
121	4	66.7	6	6	ADA61806	Ada61806 NFkB esse	194	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
122	4	66.7	6	6	ADA61776	Ada61776 IKKbeta N	195	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
123	4	66.7	7	4	AAm45417	Aam45417 H11 bindi	196	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
124	4	66.7	7	4	AAm45422	Aam45422 H11 bindi	197	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
125	4	66.7	7	5	AAm48534	Aam48534 Anti-infl	198	4	66.7	18	6	ADA61905	Ada61905 NFkB esse
126	4	66.7	8	5	AAm48535	Aam48535 Anti-infl	199	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
127	4	66.7	8	5	AAm48527	Aam48527 Anti-infl	200	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
128	4	66.7	8	6	ADA61810	Ada61810 NFkB esse	201	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
129	4	66.7	8	6	ADA61803	Ada61803 NFkB esse	202	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
130	4	66.7	9	2	ABG60423	Abg60423 Selective	203	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
131	4	66.7	9	5	AAm48533	Aam48533 Anti-infl	204	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
132	4	66.7	9	5	AAm48533	Aam48533 Anti-infl	205	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
133	4	66.7	9	5	AAm48526	Aam48526 Anti-infl	206	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
134	4	66.7	9	5	AAm48529	Aam48529 Anti-infl	207	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
135	4	66.7	9	6	ABR56837	AbR56837 Beta-3 in	208	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
136	4	66.7	9	6	ADA61808	Ada61808 NFkB esse	209	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
137	4	66.7	9	6	ADA61802	Ada61802 NFkB esse	210	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
138	4	66.7	9	6	ADA61805	Ada61805 NFkB esse	211	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
139	4	66.7	9	6	ADA61809	Ada61809 NFkB esse	212	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
140	4	66.7	9	6	ADA61805	Ada61805 NFkB esse	213	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
141	4	66.7	10	5	ABB77313	Abb77313 IKKbeta N	214	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
142	4	66.7	10	5	AAm48531	Aam48531 Anti-infl	215	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
143	4	66.7	10	5	AAm48528	Aam48528 Anti-infl	216	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
144	4	66.7	10	6	ADA61804	Ada61804 NFkB esse	217	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
145	4	66.7	10	6	ADA61807	Ada61807 NFkB esse	218	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
146	4	66.7	11	5	ABB77311	Abb77311 Human NBD	219	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
147	4	66.7	11	5	AAm48653	Aam48653 NBD pepti	220	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
148	4	66.7	11	5	AAm48506	Aam48506 Human IKK	221	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
149	4	66.7	11	5	AAm48525	Aam48525 Anti-infl	222	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
150	4	66.7	11	6	ADA61938	Ada61938 IKKbeta N	223	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
151	4	66.7	11	6	ADA61801	Ada61801 NFkB esse	224	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
152	4	66.7	12	2	AAR33675	Aar33675 HIV princ	225	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
153	4	66.7	12	6	ADA61918	Ada61918 NFkB esse	226	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
154	4	66.7	12	7	ADC28147	Adc28147 Synthetic	227	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
155	4	66.7	12	7	AAy78379	Aay78379 Human pap	228	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
156	4	66.7	13	5	AAm48640	Aam48640 Anti-infl	229	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
157	4	66.7	13	5	AAm48642	Aam48642 Anti-infl	230	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
158	4	66.7	13	5	AAm48645	Aam48645 Anti-infl	231	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
159	4	66.7	13	6	ADA61921	Ada61921 NFkB esse	232	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
160	4	66.7	13	6	ADA61916	Ada61916 NFkB esse	233	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
161	4	66.7	13	6	ADA61927	Ada61927 NFkB esse	234	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
162	4	66.7	13	6	ADA61929	Ada61929 NFkB esse	235	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
163	4	66.7	13	6	ADA61928	Ada61928 NFkB esse	236	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
164	4	66.7	14	4	AAm96947	Aam96947 Human pep	237	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
165	4	66.7	14	6	ADA61917	Ada61917 NFkB esse	238	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
166	4	66.7	14	6	ADA61938	Ada61938 NFkB esse	239	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
167	4	66.7	17	5	AAm48638	Aam48638 Anti-infl	240	4	66.7	18	6	ADA61909	Ada61909 NFkB esse
168	4	66.7	17	5	AAm48644	Aam48644 Anti-infl	241	4	66.7	18	6	ADA61924	Ada61924 NFkB esse
169	4	66.7	17	5	AAm48639	Aam48639 Anti-infl	242	4	66.7	18	6	ADA61908	Ada61908 NFkB esse
170	4	66.7	17	5	AAm48643	Aam48643 Anti-infl	243	4	66.7	18	6	ADA61922	Ada61922 NFkB esse
171	4	66.7	17	6	ADA61930	Ada61930 NFkB esse	244	4	66.7	18	6	ADA61909	Ada61909 NFkB esse

245	4	66.7	51	6	ABU07187	Abu07187 Maize SSI	318	4	66.7	94	4	AAW77186	Ram77186 Human bon
246	4	66.7	51	6	ABU07182	Abu07182 Maize SSI	319	4	66.7	94	4	AAW64361	Ram64361 Human liv
247	4	66.7	52	6	ABU07186	Abu07186 Maize SSI	320	4	66.7	94	4	ABG58809	ABG58809 Human bra
248	4	66.7	52	6	ABU07179	Abu07179 Maize Sta	321	4	66.7	94	4	ABG17509	ABG17509 Novel hum
249	4	66.7	52	6	ABU07180	Abu07180 Maize SSI	322	4	66.7	94	4	ABG17547	ABG17547 Novel hum
250	4	66.7	52	6	ABU07185	Abu07185 Maize SSI	323	4	66.7	94	5	ABG46199	ABG46199 Human pep
251	4	66.7	52	6	ABU07184	Abu07184 Maize SSI	324	4	66.7	94	6	ABP75436	ABP75436 Human sec
252	4	66.7	52	6	ABU07188	Abu07188 Maize SSI	325	4	66.7	95	4	AAW89228	AAW89228 Human imm
253	4	66.7	53	6	AAU44655	AAU44655 Propionib	326	4	66.7	95	6	ABR58357	ABR58357 Bcul040 p
254	4	66.7	53	6	ABM41174	ABM41174 Propionib	327	4	66.7	96	5	ABBI0043	ABBI0043 Human glu
255	4	66.7	54	6	AAU42648	AAU42648 Propionib	328	4	66.7	98	4	AAW95858	AAW95858 Human rep
256	4	66.7	54	6	ABM39167	ABM39167 Propionib	329	4	66.7	98	4	ABB96389	ABB96389 Human tes
257	4	66.7	55	4	AAW79292	AAW79292 Amino aci	330	4	66.7	99	2	AAW07302	AAW07302 C-termina
258	4	66.7	55	4	AAU52825	AAU52825 Propionib	331	4	66.7	99	4	AAW95002	AAW95002 Human rep
259	4	66.7	55	6	ABM49344	ABM49344 Propionib	332	4	66.7	99	4	ABB95710	ABB95710 Human tes
260	4	66.7	56	4	AAW79290	AAW79290 Amino aci	333	4	66.7	101	4	AAU59343	AAU59343 Propionib
261	4	66.7	59	2	AAW21373	AAW21373 Human HUP	334	4	66.7	101	4	AAU62311	AAU62311 Propionib
262	4	66.7	60	4	AAO04611	AAO04611 Human pol	335	4	66.7	101	6	ADA54754	ADA54754 Human pro
263	4	66.7	60	4	ABG30122	ABG30122 Novel hum	336	4	66.7	101	6	ABM55862	ABM55862 Propionib
264	4	66.7	61	4	AAW80639	AAW80639 Human hae	337	4	66.7	101	6	ABM58830	ABM58830 Propionib
265	4	66.7	63	6	ABR41192	ABR41192 Human DIT	338	4	66.7	103	2	AAW06339	AAW06339 Gliocladi
266	4	66.7	64	4	AAU48905	AAU48905 Propionib	339	4	66.7	105	4	ABG10964	ABG10964 Novel hum
267	4	66.7	64	6	ABM45424	ABM45424 Propionib	340	4	66.7	106	4	AAW84073	AAW84073 Human imm
268	4	66.7	65	4	AAU49106	AAU49106 Propionib	341	4	66.7	108	2	AAW34219	AAW34219 Streptom
269	4	66.7	65	6	ABM45625	ABM45625 Propionib	342	4	66.7	108	2	AAW55820	AAW55820 Streptom
270	4	66.7	66	4	AAU64373	AAU64373 Propionib	343	4	66.7	109	2	AAW07399	AAW07399 Chlamydia
271	4	66.7	66	6	ABM60892	ABM60892 Propionib	344	4	66.7	109	3	AAW12523	AAW12523 Zea mays
272	4	66.7	67	4	AAW94937	AAW94937 Human rep	345	4	66.7	112	5	ABP07121	ABP07121 Human ORF
273	4	66.7	67	4	AAU45676	AAU45676 Propionib	346	4	66.7	112	5	AAW49275	AAW49275 Human cel
274	4	66.7	67	4	AAU39116	AAU39116 Propionib	347	4	66.7	114	5	ABB89701	ABB89701 Human pol
275	4	66.7	67	6	ABM42195	ABM42195 Propionib	348	4	66.7	115	4	AAU19524	AAU19524 Human dia
276	4	66.7	67	6	ABM35635	ABM35635 Propionib	349	4	66.7	115	4	ABG02552	ABG02552 Novel hum
277	4	66.7	68	2	AAW12500	AAW12500 Human 5'	350	4	66.7	115	5	AAW49160	AAW49160 Human ubi
278	4	66.7	68	3	AAW56793	AAW56793 Arabidops	351	4	66.7	116	5	ABP09847	ABP09847 Human ORF
279	4	66.7	68	3	AAW60376	AAW60376 Arabidops	352	4	66.7	117	4	AAW93851	AAW93851 Human pro
280	4	66.7	68	4	ABG28346	ABG28346 Novel hum	353	4	66.7	117	5	ABG95220	ABG95220 Human nov
281	4	66.7	71	4	AAU51730	AAU51730 Propionib	354	4	66.7	117	6	ABO34414	ABO34414 Region of
282	4	66.7	71	6	ABM48249	ABM48249 Propionib	355	4	66.7	118	4	AAU49158	AAU49158 Propionib
283	4	66.7	73	4	ABG29252	ABG29252 Novel hum	356	4	66.7	118	4	AAW64019	AAW64019 Human ute
284	4	66.7	74	2	AAW40036	AAW40036 Filistata	357	4	66.7	118	4	ABG02037	ABG02037 Novel hum
285	4	66.7	74	4	AAW76325	AAW76325 Human col	358	4	66.7	118	6	ABM45677	ABM45677 Propionib
286	4	66.7	74	4	AAU52761	AAU52761 Propionib	359	4	66.7	118	7	ADC01192	ADC01192 Enterohae
287	4	66.7	74	6	ABM49280	ABM49280 Propionib	360	4	66.7	119	7	ADB65107	ADB65107 Human pro
288	4	66.7	75	4	AAU59041	AAU59041 Propionib	361	4	66.7	120	4	AAU31645	AAU31645 Novel hum
289	4	66.7	75	6	ABM55560	ABM55560 Propionib	362	4	66.7	121	2	AAW60003	AAW60003 Human end
290	4	66.7	75	6	ABU07239	ABU07239 Maize Dul	363	4	66.7	121	3	AAW03672	AAW03672 Human sec
291	4	66.7	76	3	AAW12524	AAW12524 Zea mays	364	4	66.7	122	4	AAW73933	AAW73933 Human col
292	4	66.7	77	5	ABW97840	ABW97840 Human sec	365	4	66.7	122	6	ABR39289	ABR39289 Protein s
293	4	66.7	77	5	ABW97927	ABW97927 Human sec	366	4	66.7	122	7	ADB65781	ADB65781 Human pro
294	4	66.7	81	4	AAO07074	AAO07074 Human pol	367	4	66.7	124	3	AAW12522	AAW12522 Zea mays
295	4	66.7	82	3	AAW96460	AAW96460 Partial r	368	4	66.7	125	4	ABG05086	ABG05086 Novel hum
296	4	66.7	82	4	AAW23897	AAW23897 Human EST	369	4	66.7	128	7	ADD19155	ADD19155 Lilium as
297	4	66.7	82	4	AAW80626	AAW80626 Environme	370	4	66.7	135	5	ABP34075	ABP34075 Human ORF
298	4	66.7	82	5	AAE21195	AAE21195 Human gen	371	4	66.7	135	6	ABU05089	ABU05089 Human exp
299	4	66.7	82	5	ABG64851	ABG64851 Human alb	372	4	66.7	137	6	ABP80191	ABP80191 N. gonorr
300	4	66.7	82	6	ADA56952	ADA56952 Human sec	373	4	66.7	139	3	AAW46683	AAW46683 Human 5'
301	4	66.7	82	6	ADA40803	ADA40803 Human sec	374	4	66.7	140	4	AAW16426	AAW16426 Human nov
302	4	66.7	83	4	AAU53907	AAU53907 Propionib	375	4	66.7	140	4	AAW78872	AAW78872 Human DNA
303	4	66.7	83	6	ABM50426	ABM50426 Propionib	376	4	66.7	140	6	ABG15558	ABG15558 Novel hum
304	4	66.7	84	2	AAW33719	AAW33719 Human plo	377	4	66.7	140	6	ABU55495	ABU55495 Human nov
305	4	66.7	84	4	ABW17259	ABW17259 Human ner	378	4	66.7	141	2	AAW73883	AAW73883 Human pro
306	4	66.7	86	2	AAW36020	AAW36020 Extended	379	4	66.7	141	2	AAW59770	AAW59770 Human nor
307	4	66.7	87	5	ABW97836	ABW97836 Human sec	380	4	66.7	144	3	AAW25420	AAW25420 Pinus rad
308	4	66.7	88	5	ABP01735	ABP01735 Human ORF	381	4	66.7	144	6	ABU19018	ABU19018 Protein e
309	4	66.7	88	6	ABU00805	ABU00805 S. pneumo	382	4	66.7	145	4	ABG09589	ABG09589 Novel hum
310	4	66.7	90	4	AAU40365	AAU40365 Propionib	383	4	66.7	145	6	ABP75609	ABP75609 Human sec
311	4	66.7	90	5	ABU10366	ABU10366 Human bre	384	4	66.7	146	6	ABU18616	ABU18616 Protein e
312	4	66.7	90	6	ABM36884	ABM36884 Propionib	385	4	66.7	150	4	AAU59042	AAU59042 Propionib
313	4	66.7	93	4	AAO03124	AAO03124 Human pol	386	4	66.7	150	6	ABG15892	ABG15892 Novel hum
314	4	66.7	94	4	AAW21117	AAW21117 Peptide #	387	4	66.7	150	6	ABM55561	ABM55561 Propionib
315	4	66.7	94	4	ABW43432	ABW43432 Peptide #	388	4	66.7	151	2	AAW59765	AAW59765 Human nor
316	4	66.7	94	4	AAW37320	AAW37320 Peptide #	389	4	66.7	151	4	AAW80326	AAW80326 Human hae
317	4	66.7	94	4	ABW26403	ABW26403 Protein #	390	4	66.7	153	3	AAW43922	AAW43922 Human can

391	4	66.7	154	4	AAB63563	Rab63563 Human gas	464	4	66.7	246	6	ABU02373	Abu02373 S. pneumo
392	4	66.7	158	4	ABG11618	Abg11618 Novel hum	465	4	66.7	247	2	AAW38504	Aaw38504 Streptoco
393	4	66.7	160	4	AAU43406	Aau43406 Propionib	466	4	66.7	247	2	AY85933	AY85933 S. pneumo
394	4	66.7	160	6	ABM39925	Abm39925 Propionib	467	4	66.7	247	4	AU37868	Au37868 Streptoco
395	4	66.7	160	6	ABU40249	Abu40249 Protein e	468	4	66.7	247	4	AU38029	Au38029 Streptoco
396	4	66.7	163	2	RA91595	Rar91595 PR-1 like	469	4	66.7	247	4	AB71338	Ab71338 Drosophil
397	4	66.7	163	2	AAU23944	Aau23944 Zea mays	470	4	66.7	247	6	ABU02263	Abu02263 S. pneumo
398	4	66.7	164	6	ABR47872	AbR47872 Human sec	471	4	66.7	247	6	ABU44315	Abu44315 Protein e
399	4	66.7	164	6	ABR00141	AbR00141 Human gen	472	4	66.7	249	5	ABP26263	Abp26263 Streptoco
400	4	66.7	164	7	ADC91628	Adc91628 Human sec	473	4	66.7	249	6	ABU46851	Abu46851 Protein e
401	4	66.7	164	7	ADC74263	Adc74263 Human sec	474	4	66.7	249	6	AG91045	Ag91045 C glutami
402	4	66.7	166	4	AAU93883	Aau93883 Human pol	475	4	66.7	250	4	ABU46217	Abu46217 Protein e
403	4	66.7	167	4	AAU19622	Aau19622 Human dia	476	4	66.7	251	1	AP70569	Ap70569 Sequence
404	4	66.7	168	6	ADA54238	Ada54238 Human pro	477	4	66.7	255	5	ABU23177	Abu23177 Protein e
405	4	66.7	169	4	ABB69952	Abb69952 Drosophil	478	4	66.7	257	5	ABU05566	Abu05566 M. tuberc
406	4	66.7	170	2	AAU23215	Aau23215 Amino aci	479	4	66.7	257	4	ABG18737	Abg18737 Novel hum
407	4	66.7	172	3	ABY96470	AbY96470 Rice gamm	480	4	66.7	258	4	AAU23532	Aau23532 Human EST
408	4	66.7	175	4	ABB69153	Abb69153 Drosophil	481	4	66.7	259	4	AAU23532	Aau23532 Human EST
409	4	66.7	178	6	ABU38927	Abu38927 Protein e	482	4	66.7	260	4	AAU42168	Aau42168 Human pol
410	4	66.7	179	2	AAU19847	Aau19847 B. burgdo	483	4	66.7	262	2	AAW27282	Aaw27282 Plant ste
411	4	66.7	184	2	AAU19849	Aau19849 B. burgdo	484	4	66.7	262	2	AAW27282	Aaw27282 Arabidops
412	4	66.7	184	2	AAU19849	Aau19849 B. burgdo	485	4	66.7	262	2	AAW27282	Aaw27282 Arabidops
413	4	66.7	188	4	AAU30685	Aau30685 Novel hum	486	4	66.7	266	3	AGS11383	AgS11383 Arabidops
414	4	66.7	190	2	AAU36030	Aau36030 Extended	487	4	66.7	266	3	AGS11383	AgS11383 Arabidops
415	4	66.7	190	2	AAU35924	Aau35924 Human pro	488	4	66.7	272	5	AAO20952	Aao20952 Human-N-K
416	4	66.7	190	4	AAU40382	Aau40382 Human pro	489	4	66.7	272	5	AAO20952	Aao20952 Human-N-K
417	4	66.7	191	6	ABR39942	AbR39942 Human pro	490	4	66.7	272	5	AAO20952	Aao20952 Human-N-K
418	4	66.7	191	3	AAU96459	Aau96459 Corn gamm	491	4	66.7	272	7	ADC95914	Adc95914 E. faeciu
419	4	66.7	195	6	ADA55707	Ada55707 Human pro	492	4	66.7	272	7	ADC95914	Adc95914 E. faeciu
420	4	66.7	199	4	ABG05956	Abg05956 Novel hum	493	4	66.7	273	4	ABG11759	Abg11759 Novel hum
421	4	66.7	202	7	ADB64582	Adb64582 Human pro	494	4	66.7	273	6	ABU38161	Abu38161 Protein e
422	4	66.7	203	2	AAU19846	Aau19846 B. burgdo	495	4	66.7	273	6	ABU38161	Abu38161 Protein e
423	4	66.7	203	2	AAU19848	Aau19848 B. burgdo	496	4	66.7	276	3	AGG09067	AgG09067 Arabidops
424	4	66.7	204	3	ABG36057	Abg36057 Zea mays	497	4	66.7	280	6	ABP96395	Abp96395 Nostoc pu
425	4	66.7	206	4	ABU12052	Abu12052 Human dJ8	498	4	66.7	280	6	ABP96395	Abp96395 Nostoc pu
426	4	66.7	206	6	ABP75868	Abp75868 Human sec	499	4	66.7	280	7	ADD19156	Add19156 Nostoc pu
427	4	66.7	207	3	AAU29277	Aau29277 Arabidops	500	4	66.7	280	7	ADD19156	Add19156 Nostoc pu
428	4	66.7	207	6	ABU00213	Abu00213 Human nov	501	4	66.7	281	4	ABG02036	Abg02036 Novel hum
429	4	66.7	209	4	ABG29051	Abg29051 Novel hum	502	4	66.7	281	4	ABG02036	Abg02036 Novel hum
430	4	66.7	210	4	ABG03371	Abg03371 Novel hum	503	4	66.7	281	7	AAO29691	Aao29691 Human D-a
431	4	66.7	210	5	ABP42048	Abp42048 Human ova	504	4	66.7	282	3	AGG09066	AgG09066 Human D-a
432	4	66.7	213	4	AAE00717	Aae00717 Rice BCS1	505	4	66.7	282	5	ABG97188	Abg97188 Novel hum
433	4	66.7	213	4	ABG67279	Abg67279 Amino aci	506	4	66.7	284	6	ABJ18778	Abj18778 Pseudomon
434	4	66.7	213	5	ABB83844	Abb83844 Human end	507	4	66.7	285	5	ABG97188	Abg97188 Novel hum
435	4	66.7	215	7	ADC96623	Adc96623 E. faeciu	508	4	66.7	285	5	ABG97188	Abg97188 Novel hum
436	4	66.7	217	7	ADC96623	Adc96623 E. faeciu	509	4	66.7	286	3	AAU22304	Aau22304 Corn aci
437	4	66.7	220	6	ABP56486	Abp56486 Human D-a	510	4	66.7	287	6	ABP79668	Abp79668 N. gonorr
438	4	66.7	220	7	AAO29689	Aao29689 Human D-a	511	4	66.7	290	4	ABG03255	Abg03255 Novel hum
439	4	66.7	223	2	AAW63025	Aaw63025 Theileria	512	4	66.7	292	3	AAU96463	Aau96463 Partial w
440	4	66.7	224	5	ABP41334	Abp41334 Human ova	513	4	66.7	293	3	AAU96463	Aau96463 Partial w
441	4	66.7	224	5	ABP41334	Abp41334 Human ova	514	4	66.7	294	6	ABU06977	Abu06977 Maize Sta
442	4	66.7	225	6	ABU25760	Abu25760 Protein e	515	4	66.7	295	2	AAU05562	Aau05562 Laminin -
443	4	66.7	231	4	ABU12209	Abu12209 Novel hum	516	4	66.7	295	5	ABB57248	Abb57248 Mouse isc
444	4	66.7	234	4	AAU51001	Aau51001 Propionib	517	4	66.7	295	6	ABU04658	Abu04658 Human exp
445	4	66.7	234	6	ABM47520	Abm47520 Propionib	518	4	66.7	295	6	ABU04658	Abu04658 Human exp
446	4	66.7	235	4	AAU52773	Aau52773 Propionib	519	4	66.7	295	6	ABU04659	Abu04659 Human exp
447	4	66.7	235	6	ABM49292	Abm49292 Propionib	520	4	66.7	295	6	ABU04662	Abu04662 Human exp
448	4	66.7	237	5	ABG19300	Abg19300 Novel hum	521	4	66.7	295	6	ABU04662	Abu04662 Human exp
449	4	66.7	237	5	ABG19300	Abg19300 Novel hum	522	4	66.7	295	6	ABU04662	Abu04662 Human exp
450	4	66.7	237	6	ABU32764	Abu32764 Protein e	523	4	66.7	295	6	ABU04672	Abu04672 Human exp
451	4	66.7	238	2	AAU06361	Aau06361 Gliocladi	524	4	66.7	295	6	ABU04672	Abu04672 Human exp
452	4	66.7	238	3	AAU14874	Aau14874 Amino aci	525	4	66.7	295	6	ABU04672	Abu04672 Human exp
453	4	66.7	238	3	AAU14874	Aau14874 Amino aci	526	4	66.7	295	6	ABU04672	Abu04672 Human exp
454	4	66.7	238	3	AAU14874	Aau14874 Amino aci	527	4	66.7	295	6	ABU04672	Abu04672 Human exp
455	4	66.7	239	3	AAU84331	Aau84331 Aspergill	528	4	66.7	295	6	ABU04661	Abu04661 Human exp
456	4	66.7	239	3	AAU84331	Aau84331 Aspergill	529	4	66.7	295	6	ABU04661	Abu04661 Human exp
457	4	66.7	239	3	AAU84331	Aau84331 Aspergill	530	4	66.7	295	6	ABU04661	Abu04661 Human exp
458	4	66.7	239	5	AAU77574	Aau77574 A. kawach	531	4	66.7	296	4	AAU00171	Aau00171 N-termina
459	4	66.7	239	5	AAU77574	Aau77574 A. kawach	532	4	66.7	296	4	AAU00171	Aau00171 N-termina
460	4	66.7	241	4	ABG25707	Abg25707 Novel hum	533	4	66.7	297	4	ABG18736	Abg18736 Novel hum
461	4	66.7	243	4	ABG17504	Abg17504 Novel hum	534	4	66.7	298	2	AAU13982	Aau13982 Geranylge
462	4	66.7	246	5	ABP26262	Abp26262 Streptoco	535	4	66.7	298	2	AAU13982	Aau13982 Geranylge
463	4	66.7	246	5	ABP60839	Abp60839 Caenorhab	536	4	66.7	298	2	AAU13982	Aau13982 Geranylge

537	4	66.7	298	2	AAW32470	AAW32470	Erwinia h	610	4	66.7	308	7	ADB17997	ADB17997	Human	PRO
538	4	66.7	298	5	AAO15511	AAO15511	Agromyces	611	4	66.7	308	7	ADA86680	ADA86680	Novel	hum
539	4	66.7	299	3	AAG22906	AAG22906	Arabidops	612	4	66.7	308	7	ADA87783	ADA87783	Novel	hum
540	4	66.7	299	5	ABB90876	ABB90876	Herbicida	613	4	66.7	308	7	ADA46171	ADA46171	Novel	hum
541	4	66.7	300	2	AAO7532	AAO7532	Modified	614	4	66.7	308	7	ADB28201	ADB28201	Human	PRO
542	4	66.7	300	6	ABU04666	ABU04666	Human exp	615	4	66.7	308	7	ADB28753	ADB28753	Human	PRO
543	4	66.7	301	6	ABP96390	ABP96390	Brassica	616	4	66.7	308	7	ADA76705	ADA76705	Human	PRO
544	4	66.7	301	6	ABP96389	ABP96389	Brassica	617	4	66.7	308	7	ADA88335	ADA88335	Novel	hum
545	4	66.7	302	4	ABG11344	ABG11344	Novel hum	618	4	66.7	308	7	ADA97340	ADA97340	Human	PRO
546	4	66.7	305	6	ABP96394	ABP96394	Zea mays	619	4	66.7	308	7	ADB27097	ADB27097	Human	PRO
547	4	66.7	306	4	AAE00227	AAE00227	protein e	620	4	66.7	308	7	ADB22030	ADB22030	Novel	hum
548	4	66.7	306	7	ADB91913	ADB91913	Acyltrans	621	4	66.7	308	7	ADA66721	ADA66721	Human	PRO
549	4	66.7	307	2	AAO113981	AAO113981	Geranylye	622	4	66.7	308	7	ADB22582	ADB22582	Human	PRO
550	4	66.7	307	2	AAW01119	AAW01119	Geranylye	623	4	66.7	308	7	ADB23355	ADB23355	Human	PRO
551	4	66.7	307	2	AAW00170	AAW00170	Geranylye	624	4	66.7	308	7	ADA92077	ADA92077	Novel	hum
552	4	66.7	307	2	AAW00341	AAW00341	wild type	625	4	66.7	308	7	ADB15140	ADB15140	Human	PRO
553	4	66.7	307	2	AAW32469	AAW32469	Geranylye	626	4	66.7	308	7	ADB38392	ADB38392	Novel	hum
554	4	66.7	307	4	ABB64446	ABB64446	Drosophil	627	4	66.7	308	7	ADB37840	ADB37840	Novel	hum
555	4	66.7	307	5	ABP69089	ABP69089	Human pol	628	4	66.7	308	7	ADB66312	ADB66312	Novel	hum
556	4	66.7	308	3	ABP07857	ABP07857	Arabidops	629	4	66.7	308	7	ADB89332	ADB89332	Human	PRO
557	4	66.7	308	3	AAG51382	AAG51382	Arabidops	630	4	66.7	308	7	ADB90124	ADB90124	Human	PRO
558	4	66.7	308	4	AAU12221	AAU12221	Human PRO	631	4	66.7	308	7	ADB39225	ADB39225	Novel	hum
559	4	66.7	308	6	ABO17665	ABO17665	Novel hum	632	4	66.7	308	7	ADB46848	ADB46848	Novel	hum
560	4	66.7	308	6	ABU80919	ABU80919	Human PRO	633	4	66.7	308	7	ADB86455	ADB86455	Human	PRO
561	4	66.7	308	6	ABU66619	ABU66619	Human PRO	634	4	66.7	308	7	ADB77060	ADB77060	Novel	hum
562	4	66.7	308	6	ABU59700	ABU59700	Novel sec	635	4	66.7	308	7	ADB34217	ADB34217	Human	PRO
563	4	66.7	308	6	ABO24890	ABO24890	Human sec	636	4	66.7	308	7	ADB35321	ADB35321	Human	PRO
564	4	66.7	308	6	ABU66895	ABU66895	Human sec	637	4	66.7	308	7	ADB33665	ADB33665	Human	PRO
565	4	66.7	308	6	ADA45619	ADA45619	Novel hum	638	4	66.7	308	7	ADB34769	ADB34769	Human	PRO
566	4	66.7	308	6	ADA76050	ADA76050	Human PRO	639	4	66.7	308	7	ADB35873	ADB35873	Human	PRO
567	4	66.7	308	6	ADA18700	ADA18700	Human PRO	640	4	66.7	308	7	ADB46268	ADB46268	Novel	hum
568	4	66.7	308	6	ADA61323	ADA61323	Homo sapi	641	4	66.7	308	7	ADC50141	ADC50141	Novel	hum
569	4	66.7	308	6	ADB19108	ADB19108	Novel hum	642	4	66.7	308	7	ADC71688	ADC71688	Novel	hum
570	4	66.7	308	6	ADB27649	ADB27649	Human PRO	643	4	66.7	308	7	ADC59667	ADC59667	Novel	hum
571	4	66.7	308	6	ADA86128	ADA86128	Novel hum	644	4	66.7	308	7	ADC52674	ADC52674	Novel	hum
572	4	66.7	308	6	ADB15692	ADB15692	Human PRO	645	4	66.7	308	7	ADC57028	ADC57028	Novel	hum
573	4	66.7	308	6	ADA47478	ADA47478	Human PRO	646	4	66.7	308	7	ADC60219	ADC60219	Novel	hum
574	4	66.7	308	6	ADA67273	ADA67273	Human PRO	647	4	66.7	308	7	ADC50694	ADC50694	Novel	hum
575	4	66.7	308	6	ADB30280	ADB30280	Human PRO	648	4	66.7	308	7	ADC65221	ADC65221	Human	PRO
576	4	66.7	308	6	ADA85576	ADA85576	Novel hum	649	4	66.7	308	7	ADC54319	ADC54319	Novel	hum
577	4	66.7	308	6	ADA96788	ADA96788	Human PRO	650	4	66.7	308	7	ADC53280	ADC53280	Novel	hum
578	4	66.7	308	6	ADA79092	ADA79092	Human PRO	651	4	66.7	308	7	ADC58803	ADC58803	Novel	hum
579	4	66.7	308	6	ADA87231	ADA87231	Novel hum	652	4	66.7	308	7	ADC55681	ADC55681	Novel	hum
580	4	66.7	308	6	ADB16433	ADB16433	Human PRO	653	4	66.7	308	7	ADC58251	ADC58251	Novel	hum
581	4	66.7	308	6	ADA91525	ADA91525	Novel hum	654	4	66.7	308	7	ADD02925	ADD02925	Novel	hum
582	4	66.7	308	6	ADB14588	ADB14588	Human PRO	655	4	66.7	308	7	ADC89917	ADC89917	Novel	hum
583	4	66.7	308	6	ADB18549	ADB18549	Novel hum	656	4	66.7	308	7	ADC69336	ADC69336	Human	PRO
584	4	66.7	308	6	ADA93764	ADA93764	Human PRO	657	4	66.7	308	7	ADC48225	ADC48225	Human	PRO
585	4	66.7	308	6	ADB13660	ADB13660	Novel hum	658	4	66.7	308	7	ADD09754	ADD09754	Human	PRO
586	4	66.7	308	6	ADB12972	ADB12972	Human PRO	659	4	66.7	308	7	ADD04329	ADD04329	Novel	hum
587	4	66.7	308	6	ABO43198	ABO43198	Novel hum	660	4	66.7	308	7	ADC80285	ADC80285	Novel	hum
588	4	66.7	308	6	ADA74226	ADA74226	Human PRO	661	4	66.7	308	7	ADD10792	ADD10792	Human	PRO
589	4	66.7	308	6	ADB24459	ADB24459	Human PRO	662	4	66.7	308	7	ADC47673	ADC47673	Human	PRO
590	4	66.7	308	6	ADA81983	ADA81983	Human PRO	663	4	66.7	308	7	ADC79733	ADC79733	Novel	hum
591	4	66.7	308	6	ADA74946	ADA74946	Human PRO	664	4	66.7	308	7	ADD09202	ADD09202	Human	PRO
592	4	66.7	308	6	ADA85024	ADA85024	Novel hum	665	4	66.7	308	7	ADD40915	ADD40915	Novel	hum
593	4	66.7	308	6	ADA84472	ADA84472	Novel hum	666	4	66.7	308	7	ADD52054	ADD52054	Human	PRO
594	4	66.7	308	6	ADB29728	ADB29728	Human PRO	667	4	66.7	308	7	ADD52794	ADD52794	Human	PRO
595	4	66.7	308	6	ADA80256	ADA80256	Human PRO	668	4	66.7	308	7	ADD53346	ADD53346	Novel	hum
596	4	66.7	308	6	ADA75498	ADA75498	Human PRO	669	4	66.7	308	7	ADD51502	ADD51502	Human	PRO
597	4	66.7	308	6	ADA46723	ADA46723	Human PRO	670	4	66.7	308	7	ADD02301	ADD02301	Human	PRO
598	4	66.7	308	6	ADB25019	ADB25019	Human PRO	671	4	66.7	308	7	ADD01735	ADD01735	Novel	hum
599	4	66.7	308	6	ADA93195	ADA93195	Human PRO	672	4	66.7	308	7	ADD53917	ADD53917	Novel	hum
600	4	66.7	308	6	ADB26545	ADB26545	Human PRO	673	4	66.7	308	7	ADD92234	ADD92234	Human	PRO
601	4	66.7	308	6	ADB30832	ADB30832	Human PRO	674	4	66.7	308	7	ADD91130	ADD91130	Human	PRO
602	4	66.7	308	6	ADA60760	ADA60760	Homo sapi	675	4	66.7	308	7	ADE03744	ADE03744	Human	PRO
603	4	66.7	308	6	ADB23907	ADB23907	Human PRO	676	4	66.7	308	7	ADE32041	ADE32041	Novel	hum
604	4	66.7	308	6	ADA96236	ADA96236	Human PRO	677	4	66.7	308	7	ADE21973	ADE21973	Human	PRO
605	4	66.7	308	6	ADA80808	ADA80808	Human PRO	678	4	66.7	308	7	ADD79197	ADD79197	Human	PRO
606	4	66.7	308	6	ADA95684	ADA95684	Human PRO	679	4	66.7	308	7	ADE41733	ADE41733	Human	PRO
607	4	66.7	308	6	ADB25993	ADB25993	Human PRO	680	4	66.7	308	7	ADE17550	ADE17550	Human	PRO
608	4	66.7	308	6	ADB21478	ADB21478	Novel hum	681	4	66.7	308	7	ADD91682	ADD91682	Human	PRO
609	4	66.7	308	7	ADA77257	ADA77257	Human PRO	682	4	66.7	308	7	ADE33145	ADE33145	Novel	hum

683	4	66.7	308	7	ADE33697	Novel hum	756	4	66.7	346	2	AAR51473	Aar51473	ptsS gene
684	4	66.7	308	7	ADD79749	Human PRO	757	4	66.7	346	2	AAR60641	Aar60641	ptsS vari
685	4	66.7	308	7	ADD92786	Human PRO	758	4	66.7	346	2	AAR60642	Aar60642	ptsS vari
686	4	66.7	308	7	ADE19206	Human PRO	759	4	66.7	346	2	AAR60643	Aar60643	ptsS vari
687	4	66.7	308	7	ADE18654	Human PRO	760	4	66.7	346	2	AAR60647	Aar60647	ptsS vari
688	4	66.7	308	7	ADE42850	Human PRO	761	4	66.7	346	2	AAR60640	Aar60640	ptsS vari
689	4	66.7	308	7	ADD95639	Human PRO	762	4	66.7	346	2	AAR60644	Aar60644	ptsS vari
690	4	66.7	308	7	ADE22525	Human PRO	763	4	66.7	346	2	AAR60653	Aar60653	ptsS vari
691	4	66.7	308	7	ADD78643	Human PRO	764	4	66.7	346	2	AAR60648	Aar60648	ptsS vari
692	4	66.7	308	7	ADE32593	Novel hum	765	4	66.7	346	2	AAR60651	Aar60651	ptsS vari
693	4	66.7	308	7	ADD80301	Human PRO	766	4	66.7	346	2	AAR60652	Aar60652	ptsS vari
694	4	66.7	308	7	ADD89329	Human PRO	767	4	66.7	346	2	AAR60654	Aar60654	ptsS vari
695	4	66.7	308	7	ADE40613	Human PRO	768	4	66.7	346	2	AAR60646	Aar60646	ptsS vari
696	4	66.7	308	7	ADE04412	Human PRO	769	4	66.7	346	2	AAR60650	Aar60650	ptsS vari
697	4	66.7	308	7	ADE04412	Human PRO	770	4	66.7	346	2	AAG98332	Aag98332	Escherich
698	4	66.7	308	8	ADC80837	Novel hum	771	4	66.7	346	2	AAG72010	Aag72010	HSV-2 str
699	4	66.7	308	8	ADD76285	Human PRO	772	4	66.7	347	4	AU68594	Au68594	Human nov
700	4	66.7	308	8	ADD87649	Human PRO	773	4	66.7	347	4	ABG28895	Abg28895	Novel hum
701	4	66.7	308	8	ADD86053	Human PRO	774	4	66.7	347	6	ABP96381	Abp96381	Brassica
702	4	66.7	308	8	ADD75501	Human PRO	775	4	66.7	347	6	ABP96380	Abp96380	Brassica
703	4	66.7	308	8	ADE23077	Human PRO	776	4	66.7	347	6	ABP56485	Abp56485	Human D-a
704	4	66.7	308	8	ADE23629	Human PRO	777	4	66.7	347	6	ABP56491	Abp56491	Human D-a
705	4	66.7	308	8	ADE24272	Human PRO	778	4	66.7	347	6	ABP56491	Abp56491	Human D-a
706	4	66.7	308	8	ADD87097	Human PRO	779	4	66.7	347	6	AAO23078	Aao23078	Human D-a
707	4	66.7	308	8	ADE88963	Human PRO	780	4	66.7	347	6	AAO23074	Aao23074	Human D-a
708	4	66.7	308	8	ADE18102	Human PRO	781	4	66.7	347	6	AAO23075	Aao23075	Human D-a
709	4	66.7	308	8	ADE88411	Human PRO	782	4	66.7	347	6	AAO29694	Aao29694	Human D-a
710	4	66.7	310	5	AAU97833	Fucose-sp	783	4	66.7	347	7	AAO29688	Aao29688	Human D-a
711	4	66.7	310	6	ABP96386	Tagetes e	784	4	66.7	347	7	AAO29697	Aao29697	Alternati
712	4	66.7	310	7	ADD19153	Tagetes e	785	4	66.7	347	7	ADD19148	Add19148	Brassica
713	4	66.7	311	6	ABP96393	Tagetes e	786	4	66.7	347	7	ADD19147	Add19147	Brassica
714	4	66.7	313	3	ABG09396	Novel hum	787	4	66.7	348	2	AAW95017	Aaw95017	Arabidops
715	4	66.7	314	4	ABG09396	Novel hum	788	4	66.7	348	3	AAW77937	Aaw77937	A. thalia
716	4	66.7	314	6	ABM69332	Photorhab	789	4	66.7	348	3	AAO7856	Aao7856	Arabidops
717	4	66.7	317	2	AAW95016	Synechocy	790	4	66.7	348	3	AAO7856	Aao7856	Arabidops
718	4	66.7	317	2	AAU23764	A carboxy	791	4	66.7	348	5	AAO7856	Aao7856	Arabidops
719	4	66.7	317	2	AAU23764	Carboxyme	792	4	66.7	348	5	ABG11452	Abg11452	Herbicida
720	4	66.7	317	3	AAU56814	T. mariti	793	4	66.7	348	5	ABG11452	Abg11452	Herbicida
721	4	66.7	317	3	AAU56814	T. mariti	794	4	66.7	348	5	ABG11452	Abg11452	Herbicida
722	4	66.7	317	6	ABP56759	Thermotog	795	4	66.7	348	6	ABP96375	Abp96375	A. thalia
723	4	66.7	317	6	ABP96397	Synechocy	796	4	66.7	348	6	ABP96374	Abp96374	A. thalia
724	4	66.7	319	5	ABP74092	Candida a	797	4	66.7	350	3	ADD19141	Add19141	Arabidops
725	4	66.7	319	5	ABP28906	Streptoco	798	4	66.7	350	3	AAU23394	Aau23394	Streptomy
726	4	66.7	324	5	AAU76438	Novel des	799	4	66.7	351	3	AAU23394	Aau23394	Streptomy
727	4	66.7	325	6	ABU44241	Novel hum	800	4	66.7	351	3	AAU23394	Aau23394	Streptomy
728	4	66.7	326	4	ABG25708	Novel hum	801	4	66.7	351	3	AAU23394	Aau23394	Streptomy
729	4	66.7	328	3	AAU84620	Novel hum	802	4	66.7	352	6	ABP96377	Abp96377	Zeae may
730	4	66.7	329	4	ABG16554	Protein e	803	4	66.7	352	6	ABP96377	Abp96377	Zeae may
731	4	66.7	329	4	ABG16554	Protein e	804	4	66.7	353	6	ABP96377	Abp96377	Zeae may
732	4	66.7	331	3	AAU29037	Streptoco	805	4	66.7	354	6	ABP96387	Abp96387	Sorghum b
733	4	66.7	332	3	AAU29037	Streptoco	806	4	66.7	354	6	ABP96387	Abp96387	Sorghum b
734	4	66.7	332	4	ABG44324	Drosophil	807	4	66.7	354	7	ADD19154	Add19154	Sorghum b
735	4	66.7	332	4	ABG02033	Novel hum	808	4	66.7	354	7	ADD19154	Add19154	Sorghum b
736	4	66.7	333	4	AAU19629	Human nov	809	4	66.7	354	7	ADD19154	Add19154	Sorghum b
737	4	66.7	333	5	ABP47849	Human pol	810	4	66.7	354	7	ADD19154	Add19154	Sorghum b
738	4	66.7	333	5	ADC10811	Human ext	811	4	66.7	354	7	ADD19154	Add19154	Sorghum b
739	4	66.7	333	7	ADC94414	E. faeciu	812	4	66.7	354	7	ADD19154	Add19154	Sorghum b
740	4	66.7	336	2	AAW80692	S. pneumu	813	4	66.7	354	7	ADD19154	Add19154	Sorghum b
741	4	66.7	336	4	AAU37859	Streptoco	814	4	66.7	354	7	ADD19154	Add19154	Sorghum b
742	4	66.7	336	4	AAU37859	Streptoco	815	4	66.7	354	7	ADD19154	Add19154	Sorghum b
743	4	66.7	336	6	AAE24232	Streptomy	816	4	66.7	354	7	ADD19154	Add19154	Sorghum b
744	4	66.7	336	6	ABP91638	Streptoco	817	4	66.7	354	7	ADD19154	Add19154	Sorghum b
745	4	66.7	336	6	ABU46229	Protein e	818	4	66.7	354	7	ADD19154	Add19154	Sorghum b
746	4	66.7	337	3	AAU90999	S. venezu	819	4	66.7	354	7	ADD19154	Add19154	Sorghum b
747	4	66.7	337	3	AAU77184	Amino aci	820	4	66.7	354	7	ADD19154	Add19154	Sorghum b
748	4	66.7	337	3	AAU18651	Novel hum	821	4	66.7	354	7	ADD19154	Add19154	Sorghum b
749	4	66.7	337	3	AAU67215	ORF 14 en	822	4	66.7	354	7	ADD19154	Add19154	Sorghum b
750	4	66.7	337	5	ABP90151	Human pol	823	4	66.7	354	7	ADD19154	Add19154	Sorghum b
751	4	66.7	337	6	ABG1675	Protein s	824	4	66.7	354	7	ADD19154	Add19154	Sorghum b
752	4	66.7	337	6	ADA09414	S. venezu	825	4	66.7	354	7	ADD19154	Add19154	Sorghum b
753	4	66.7	339	5	ABP41586	Human ova	826	4	66.7	354	7	ADD19154	Add19154	Sorghum b
754	4	66.7	343	4	AAU35251	Enterococ	827	4	66.7	354	7	ADD19154	Add19154	Sorghum b
755	4	66.7	346	2	AAR60645	ptsS vari	828	4	66.7	354	7	ADD19154	Add19154	Sorghum b

829	4	66.7	396	6	ABU34229	Abu34229 Protein e	902	4	66.7	459	6	ABR64168	AbR64168 Aspergill
830	4	66.7	397	4	AAE00850	Aae00850 Human nov	903	4	66.7	459	6	ABR64134	AbR64134 Aspergill
831	4	66.7	398	6	ABG99979	AbG99979 Human nov	904	4	66.7	459	6	ABR64140	AbR64140 Aspergill
832	4	66.7	401	2	AAE10996	Aae10996 Xenopus B	905	4	66.7	459	6	ABR64160	AbR64160 Aspergill
833	4	66.7	402	5	AAO19402	Aao19402 Human mol	906	4	66.7	459	6	ABR64161	AbR64161 Aspergill
834	4	66.7	403	6	ABU96672	Abu96672 Human nuc	907	4	66.7	459	6	ABR64170	AbR64170 Aspergill
835	4	66.7	404	3	ABR32501	AbR32501 S. lavend	908	4	66.7	459	6	ABR64138	AbR64138 Aspergill
836	4	66.7	404	4	ABG12109	AbG12109 Novel hum	909	4	66.7	459	6	ABR64155	AbR64155 Aspergill
837	4	66.7	404	5	ABP66007	AbP66007 Bifidobac	910	4	66.7	459	6	ABR64169	AbR64169 Aspergill
838	4	66.7	404	7	ADB80207	AdB80207 Mycobacte	911	4	66.7	459	6	ABR64164	AbR64164 Aspergill
839	4	66.7	404	7	ADE10273	Ade10273 S. lavend	912	4	66.7	459	6	ABR64141	AbR64141 Aspergill
840	4	66.7	405	3	RAY32310	Ray32310 Soybean a	913	4	66.7	459	6	ABR64128	AbR64128 Wild type
841	4	66.7	406	6	ABO06222	AbO06222 Novel hum	914	4	66.7	459	6	ABR64172	AbR64172 Aspergill
842	4	66.7	410	3	AAE00849	Aae00849 Human nov	915	4	66.7	459	6	ABR64135	AbR64135 Aspergill
843	4	66.7	410	4	AAE00849	Aae00849 Human nov	916	4	66.7	459	6	ABR64165	AbR64165 Aspergill
844	4	66.7	411	4	AAU54878	Aau54878 Propionib	917	4	66.7	459	6	ABR64167	AbR64167 Aspergill
845	4	66.7	411	6	ABM51397	AbM51397 Propionib	918	4	66.7	459	6	ABR64175	AbR64175 Aspergill
846	4	66.7	414	4	AAE00845	Aae00845 Human nov	919	4	66.7	459	6	ABR64145	AbR64145 Aspergill
847	4	66.7	417	4	ABR67072	AbR67072 Drosophil	920	4	66.7	459	6	ABR64133	AbR64133 Aspergill
848	4	66.7	417	4	ABR67073	AbB67073 Drosophil	921	4	66.7	459	6	ABR64158	AbR64158 Aspergill
849	4	66.7	417	4	ABR62824	AbB62824 Drosophil	922	4	66.7	459	6	ABR64174	AbR64174 Aspergill
850	4	66.7	418	4	ABG14153	AbG14153 Novel hum	923	4	66.7	459	6	ABR64131	AbR64131 Aspergill
851	4	66.7	418	4	ABG03637	AbG03637 Novel hum	924	4	66.7	459	6	ABR64137	AbR64137 Aspergill
852	4	66.7	418	4	ABG07575	AbG07575 Novel hum	925	4	66.7	459	6	ABR64162	AbR64162 Aspergill
853	4	66.7	418	4	ABG07713	AbG07713 Novel hum	926	4	66.7	459	6	ABR64146	AbR64146 Aspergill
854	4	66.7	420	3	AAE00849	Aae00849 Human nov	927	4	66.7	459	6	ABR64163	AbR64163 Aspergill
855	4	66.7	423	5	ABP99400	AbP99400 Arabidops	928	4	66.7	459	6	ABR64136	AbR64136 Aspergill
856	4	66.7	425	4	ABG27494	AbG27494 Novel hum	929	4	66.7	459	6	ABR64143	AbR64143 Aspergill
857	4	66.7	425	4	ABG08503	AbG08503 Novel hum	930	4	66.7	459	6	ABR64154	AbR64154 Aspergill
858	4	66.7	426	4	ABR70789	AbR70789 N. magada	931	4	66.7	470	6	ABR64166	AbR64166 Aspergill
859	4	66.7	429	4	ABR95767	AbR95767 Human pro	932	4	66.7	470	6	ABU24443	AbU24443 Protein e
860	4	66.7	429	7	ABD74319	AbD74319 Mycobacte	933	4	66.7	474	2	AAE080507	Aae080507 S. livida
861	4	66.7	432	4	ABG19159	AbG19159 Novel hum	934	4	66.7	474	7	ABD74569	AbD74569 Mycobacte
862	4	66.7	433	2	AAW36029	Aaw36029 Protein e	935	4	66.7	476	6	ABU47353	AbU47353 Protein e
863	4	66.7	433	2	AAW1060	Aaw1060 Multiple	936	4	66.7	477	4	ABR81181	AbR81181 Transglut
864	4	66.7	433	5	ABP65809	AbP65809 Bifidobac	937	4	66.7	477	6	ABU07392	AbU07392 Foreign p
865	4	66.7	433	5	ABR84376	AbR84376 MSRV-1 as	938	4	66.7	480	6	ABR64129	AbR64129 Aspergill
866	4	66.7	434	6	ABU41213	AbU41213 Protein e	939	4	66.7	481	7	ABR81195	AbR81195 Aspergill
867	4	66.7	439	4	AAE00240	Aae00240 Taxus cus	940	4	66.7	481	4	ABG29555	AbG29555 Novel hum
868	4	66.7	439	5	ABR79398	AbB79398 Taxane sy	941	4	66.7	482	6	ABR64130	AbR64130 Aspergill
869	4	66.7	439	6	ABR82996	AbB82996 T. cupid	942	4	66.7	483	2	AAW82550	Aaw82550 Human LIR
870	4	66.7	439	7	ABR91939	AbR91939 Acyltrans	943	4	66.7	483	3	ABU04175	AbU04175 Leukocyte
871	4	66.7	440	4	AAU69493	Aau69493 Human pur	944	4	66.7	483	7	ABR44282	AbR44282 Human leu
872	4	66.7	441	5	ABR91785	AbB91785 Herbicida	945	4	66.7	484	4	AAU34864	Aau34864 E. coli c
873	4	66.7	444	4	ABR81163	AbB81163 Transglut	946	4	66.7	484	6	ABU28873	AbU28873 Protein e
874	4	66.7	445	7	ADD47439	AbD47439 Rat Prote	947	4	66.7	489	6	ABU09066	AbU09066 Mycobacte
875	4	66.7	447	6	ABU19837	AbU19837 Protein e	948	4	66.7	489	6	ABU09068	AbU09068 Mycobacte
876	4	66.7	449	6	ABM15831	AbM15831 Mycobacte	949	4	66.7	489	6	ABU09062	AbU09062 Mycobacte
877	4	66.7	451	4	AAE00844	Aae00844 Human nov	950	4	66.7	489	6	ABU09067	AbU09067 Mycobacte
878	4	66.7	452	5	ABR92178	AbB92178 Herbicida	951	4	66.7	489	6	ABU09063	AbU09063 Mycobacte
879	4	66.7	452	7	ADC01384	AdC01384 Enterohae	952	4	66.7	489	6	ABU09064	AbU09064 Mycobacte
880	4	66.7	453	4	ABR58304	AbB58304 Drosophil	953	4	66.7	489	6	ABU09065	AbU09065 Mycobacte
881	4	66.7	457	4	AAU61200	Aau61200 Propionib	954	4	66.7	489	6	ABU09065	AbU09065 Mycobacte
882	4	66.7	457	6	ABM57719	AbM57719 Propionib	955	4	66.7	489	6	ABU09062	AbU09062 Mycobacte
883	4	66.7	461	6	ABU24727	AbU24727 Protein e	956	4	66.7	489	6	ABU09067	AbU09067 Mycobacte
884	4	66.7	464	4	AAE00843	Aae00843 Human nov	957	4	66.7	495	4	ABG62159	AbG62159 Human gen
885	4	66.7	464	5	ABR49506	AbB49506 Listeria	958	4	66.7	495	5	ABG63555	AbG63555 Human alb
886	4	66.7	464	6	ABU32474	AbU32474 Protein e	959	4	66.7	495	5	ABU40304	AbU40304 Protein e
887	4	66.7	464	6	ABU25468	AbU25468 Protein e	960	4	66.7	497	4	ABG03007	AbG03007 Novel hum
888	4	66.7	466	5	AAU79040	Aau79040 Human imm	961	4	66.7	497	6	ABP76773	AbP76773 N. gonorr
889	4	66.7	468	4	ABR71291	AbB71291 Drosophil	962	4	66.7	498	5	ABP43865	AbP43865 Human mRN
890	4	66.7	469	5	ABP35645	AbP35645 Fungal ZB	963	4	66.7	498	7	ABU61938	AbU61938 Human ful
891	4	66.7	469	6	ABR64171	AbR64171 Aspergill	964	4	66.7	501	4	ABR68273	AbR68273 Amino aci
892	4	66.7	469	6	ABR64132	AbR64132 Aspergill	965	4	66.7	503	3	AAE96751	Aae96751 A. terreu
893	4	66.7	469	6	ABR64142	AbR64142 Aspergill	966	4	66.7	503	5	ABP35644	AbP35644 Fungal ZB
894	4	66.7	469	6	ABR64144	AbR64144 Aspergill	967	4	66.7	503	3	ABP35644	AbP35644 Fungal ZB
895	4	66.7	469	6	ABR64147	AbR64147 Aspergill	968	4	66.7	512	4	ABG07679	AbG07679 Novel hum
896	4	66.7	469	6	ABR64148	AbR64148 Aspergill	969	4	66.7	516	4	AAU46381	Aau46381 Propionib
897	4	66.7	469	6	ABR64152	AbR64152 Aspergill	970	4	66.7	516	5	ABM42900	AbM42900 Propionib
898	4	66.7	469	6	ABR64173	AbR64173 Aspergill	971	4	66.7	517	5	ABR92214	AbB92214 Herbicida
899	4	66.7	469	6	ABR64156	AbR64156 Aspergill	972	4	66.7	518	4	ABG13534	AbG13534 Novel hum
900	4	66.7	469	6	ABR64157	AbR64157 Aspergill	973	4	66.7	519	4	ABG4659	AbG4659 Hydroxyin
901	4	66.7	469	6	ABR64159	AbR64159 Aspergill	974	4	66.7	523	5	ABP67995	AbP67995 Human col

975 Abp78692 N. gonorr
976 Abue1933 Human Hiw
977 Abg09393 Novel hum
978 Abg20264 Novel hum
979 Aay33686 S. erythr
980 Aay33686 S. erythr
981 Aay33686 S. erythr
982 Aay33686 S. erythr
983 Aay33686 S. erythr
984 Aay33686 S. erythr
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996 Aay33686 S. erythr
997 Aay33686 S. erythr
998 Aay33686 S. erythr
999 Aay33686 S. erythr
1000 Aay33686 S. erythr

ALIGNMENTS

RESULT 1
ID AAM48538 standard; peptide; 6 AA.
AC AAM48538;
XX
XX
XX 20-MAR-2002 (first entry)
XX Anti-inflammatory peptide SEQ ID NO 41.
XX
XX Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;
XX antirheumatic; dermatologic; neuroprotective; antiatherosclerotic;
XX immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;
XX cytokine; NKkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (UYVA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
XX fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
XX activation, and for treating asthma, lung inflammation, psoriasis.
XX

PS Claim 6; Page 61; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatologic, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiasthmatic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, bursitis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, multiple sclerosis, diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies, eczema,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 6; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
Db 1 ADWSWA 6
RESULT 2
AAM48570
ID AAM48570 standard; peptide; 6 AA.
XX
XX AAM48570;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 73.
XX
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NKkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
XX
XX 02-MAY-2000; 2000US-0201261P.
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XX 22-AUG-2000; 2000US-00643260.
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XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX

PT Novel antiinflammatory compound comprising membrane translocation domain
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 PT activation, and for treating asthma, lung inflammation, psoriasis.
 XX
 PS Claim 6; Page 62; 89pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
 CC antiinflammatory compounds have antiasthmatic, cytotstatic, antipsoriatic,
 CC antiinflammatory, antiarthritic, osteopathic, antibacterial,
 CC immunosuppressive, dermatological, neuroprotective, nootropic,
 CC antiatherosclerotic, virucide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 CC viral infections; and ataxia telangiectasia. The compounds are also
 CC useful for treating pro-inflammatory responses such as allergies,
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 CC sunburn, aging and arthritis
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
 Db 1 ADMSWA 6

RESULT 3

ADA61814
 ID ADA61814 standard; peptide; 6 AA.

XX
 AC ADA61814;

XX
 DT 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #14.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.
 PA (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.

XX Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADMSWA 6
 Db 1 ADMSWA 6

RESULT 4

ADA61846
 ID ADA61846 standard; peptide; 6 AA.

XX
 AC ADA61846;

XX
 DT 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #46.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX (FIND/) FINDEIS M A.

XX (PHIL/) PHILLIPS K.

XX (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

DR WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding

PT sequence.

XX

XX Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The

CC compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 6; Length 6;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

DB 1 ADWSWA 6

RESULT 5

AAW48574

ID AAW48574 standard; peptide; 7 AA.

XX

XX AAW48574;

XX

XX 20-MAR-2002 (first entry)

XX

XX Anti-inflammatory peptide SEQ ID NO 77.

XX

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX

XX Synthetic.

XX

XX WO200183554-A2.

XX

XX 08-NOV-2001.

XX

XX 02-MAY-2001; 2001WO-US014346.

XX

XX 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX

XX (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX

XX WPI; 2002-121889/16.

XX

XX Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX

XX Claim 6; Page 62; 88pp; English.

XX

CC The invention relates to an antiinflammatory compound (especially

CC AAW48628-AAW48645), comprising a membrane translocation domain (AAW48620-

CC AAW48627 or AAW48646-AAW48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAW48525-AAW48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antiinflammatory, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and antiallergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

CC for treating inflammatory disorders, e.g. asthma, lung inflammation or

CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as

CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;

CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;

CC viral infections; and ataxia telangiectasia. The compounds are also

CC useful for treating pro-inflammatory responses such as allergies,

CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,

CC sunburn, aging and arthritis

XX

XX Sequence 7 AA;

Query Match 100.0%; Score 6; DB 5; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6

DB 1 ADWSWA 6

RESULT 6

ADA61850

ID ADA61850 standard; peptide; 7 AA.

XX

XX ADA61850;

XX

XX 20-NOV-2003 (first entry)

XX

XX NFkB essential modulator (NEMO) binding peptide #50.

XX

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX

XX Unidentified.

OS

XX US2003054999-A1.

XX

XX 20-MAR-2003.

XX

XX 02-MAY-2001; 2001US-00847946.

PF

XX 02-MAY-2000; 2000US-0201261P.

PR

XX (MAYN/) MAY M J.

PA (GHOS/) GHOSH S.

PA (FIND/) FINDEIS M A.

PA (PHIL/) PHILLIPS K.

PA (HANN/) HANNIG G.

XX

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX

XX WPI; 2003-596541/56.

DR

XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX Claim 6; Page 23; 37pp; English.
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX Sequence 7 AA;
SQ
Query Match 100.0%; Score 6; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADMSWA 6
Db 1 ADMSWA 6
RESULT 7
AAM48575
ID AAM48575 standard; peptide; 8 AA.
XX AC AAM48575;
XX DT 20-MAR-2002 (first entry)
XX DE Anti-inflammatory peptide SEQ ID NO 78.
XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX OS Synthetic.
XX PN WO200183554-A2.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US014346.
XX PR 02-MAY-2000; 2000US-0201261P.
XX PR 22-AUG-2000; 2000US-00643260.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYVA) UNIV YALE.
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX DR WPI; 2002-121889/16.
XX XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX PS Claim 6; Page 62; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, neutropic,
CC antiatherosclerotic, virucide and anti-allergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 6; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADMSWA 6
Db 1 ADMSWA 6
RESULT 8
AAM48567
ID AAM48567 standard; peptide; 8 AA.
XX AC AAM48567;
XX DT 20-MAR-2002 (first entry)
XX DE Anti-inflammatory peptide SEQ ID NO 70.
XX KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX OS Synthetic.
XX PN WO200183554-A2.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US014346.
XX PR 02-MAY-2000; 2000US-0201261P.
XX PR 22-AUG-2000; 2000US-00643260.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PA (UYVA) UNIV YALE.
XX PI May MJ, Ghosh S, Findeis MA, Phillips K;
XX DR WPI; 2002-121889/16.
XX XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.

PI	May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX	
XX	WPI; 2003-596541/56.
XX	
XX	New compound for diagnosing or treating inflammatory disorders, e.g.
PT	asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT	cancer, comprises a membrane translocation domain and a NEMO binding
PT	sequence.
XX	
XX	Claim 6; Page 23; 37pp; English.
XX	
XX	The invention describes an anti-inflammatory compound comprising (1). The
CC	compound is useful for diagnosing or treating inflammatory disorders,
CC	such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC	inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC	systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC	Alzheimer's disease or viral infection. This is the amino acid sequence
CC	of an anti-inflammatory peptide that binds to, and down-regulates,
CC	necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX	
XX	
XX	Sequence 8 AA;
XX	
XX	Query Match 100.0%; Score 6; DB 6; Length 8;
XX	Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1 ADMSWA 6
XX	
DB	1 ADMSWA 6
XX	
XX	
XX	RESULT 10
XX	ADA61843
ID	ADA61843 standard; peptide; 8 AA.
XX	
XX	ADA61843;
XX	
XX	20-NOV-2003 (first entry)
XX	
XX	NFkB essential modulator (NEMO) binding peptide #43.
XX	
XX	NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW	antiinflammatory; antiachmatic; antipsoriatic; antirheumatic;
KW	antiarthritic; osteoprotective; antibacterial; immunosuppressive;
KW	dermatological; neuroprotective; cytostatic; nontoxic; virucide;
KW	gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW	psoriasis; rheumatoid arthritis; osteoarthritis;
KW	inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW	systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW	Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW	necrosis factor kappa B essential modulator.
XX	
OS	Unidentified.
XX	
XX	US2003054999-A1.
XX	
XX	20-MAR-2003.
XX	
XX	02-MAY-2001; 2001US-00847946.
XX	
XX	02-MAY-2000; 2000US-0201261P.
XX	
XX	(MAYN/) MAY M J.
PA	(GHOS/) GHOSH S.
PA	(FIND/) FINDEIS M A.
PA	(PHIL/) PHILLIPS K.
PA	(HANN/) HANNIG G.
XX	
XX	
PI	May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX	
XX	WPI; 2003-596541/56.
XX	
XX	New compound for diagnosing or treating inflammatory disorders, e.g.
PT	

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
XX sequence.
PS Claim 6; Page 23; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ Sequence 8 AA;
Query Match 100.0%; Score 6; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 3 ADWSWA 8
|||||
RESULT 11
AAM48573
ID AAM48573 standard; peptide; 9 AA.
XX
XX AAM48573;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 76.
XX
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRACIS PHARM INC.
XX
XX (UYA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, antiallergic,
CC antiatherosclerotic, virucide and antiinflammatory activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
XX sunburn, aging and arthritis
XX
SQ Sequence 9 AA;
Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSWA 6
Db 2 ADWSWA 7
|||||
RESULT 12
AAM48566
ID AAM48566 standard; peptide; 9 AA.
XX
XX AAM48566;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 69.
XX
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRACIS PHARM INC.
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XX (UYA) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT activation, and for treating asthma, lung inflammation, psoriasis.
XX
XX Claim 6; Page 62; 88pp; English.

Mon Jul 26 09:11:20 2004

fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.

Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and anti-allergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 1 ADWSWA 6

RESULT 14
AAM48572
ID AAM48572 standard; peptide; 9 AA.

AC AAM48572;

XX 20-MAR-2002 (first entry)

DT Anti-inflammatory peptide SEQ ID NO 75.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
DE antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

FN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and anti-allergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 9 AA;

Query Match 100.0%; Score 6; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
| | | | |
Db 1 ADWSWA 6

RESULT 13
AAM48569
ID AAM48569 standard; peptide; 9 AA.

AC AAM48569;

XX 20-MAR-2002 (first entry)

DT Anti-inflammatory peptide SEQ ID NO 72.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
DE antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

PN 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

PR 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

PA (UYA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain

XX WPI; 2002-121889/16.
 XX Novel anti-inflammatory compound comprising membrane translocation domain
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 PT activation, and for treating asthma, lung inflammation, psoriasis.
 XX
 XX Claim 6; Page 62; 89pp; English.
 XX
 XX The invention relates to an anti-inflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
 CC anti-inflammatory compounds have antiasthmatic, cytotostatic, antipsoriatic,
 CC anti-rheumatic, antiarthritic, osteoprotective, antibacterial,
 CC immunosuppressive, dermatological, neuroprotective, nootropic,
 CC antiatherosclerotic, virucide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of I-kappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
 CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
 CC viral infections; and ataxia telangiectasia. The compounds are also
 CC useful for treating pro-inflammatory responses such as allergies,
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
 CC sunburn, aging and arthritis
 XX Sequence 9 AA;
 SQ

Query Match 100.0%; Score 6; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
 |||||
 Db 3 ADWSWA 8

RESULT 15
 ADA61848
 ID ADA61848 standard; peptide; 9 AA.
 XX
 AC ADA61848;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE NFkB essential modulator (NEMO) binding peptide #48.
 XX
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytotostatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.
 XX
 OS Unidentified.
 XX
 XX US2003054999-A1.
 PN
 XX
 PD 20-MAR-2003.
 XX
 XX 02-MAY-2001; 2001US-00847946.
 XX
 XX 02-MAY-2000; 2000US-0201261P.
 XX
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 PF (FIND/) FINDEIS M A.
 XX
 XX 02-MAY-2000; 2000US-0201261P.
 PR (PHIL/) PHILLIPS K.
 XX (HANN/) HANNIG G.

PA (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 PA (FIND/) FINDEIS M A.
 PA (PHIL/) PHILLIPS K.
 PA (HANN/) HANNIG G.
 XX
 PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 DR
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 XX
 XX Claim 6; Page 23; 37pp; English.
 PS
 XX The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 6; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
 |||||
 Db 3 ADWSWA 8

RESULT 16
 ADA61841
 ID ADA61841 standard; peptide; 9 AA.
 XX
 AC ADA61841;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE NFkB essential modulator (NEMO) binding peptide #41.
 XX
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytotostatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.
 XX
 OS Unidentified.
 XX
 XX US2003054999-A1.
 PN
 XX
 PD 20-MAR-2003.
 XX
 XX 02-MAY-2001; 2001US-00847946.
 XX
 XX 02-MAY-2000; 2000US-0201261P.
 XX
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 PF (FIND/) FINDEIS M A.
 XX
 XX 02-MAY-2000; 2000US-0201261P.
 PR (PHIL/) PHILLIPS K.
 XX (HANN/) HANNIG G.

Mon Jul 26 09:11:20 2004

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 XX PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 XX PT cancer, comprises a membrane translocation domain and a NEMO binding
 XX PT sequence.
 XX
 XX Claim 6; Page 23; 37pp; English.
 XX
 XX The invention describes an anti-inflammatory compound comprising (I). The
 XX compound is useful for diagnosing or treating inflammatory disorders,
 XX such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 XX inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 XX systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 XX Alzheimer's disease or viral infection. This is the amino acid sequence
 XX of an anti-inflammatory peptide that binds to, and down-regulates,
 XX necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 100.0%; Score 6; DB 6; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ADWSWA 6
 XX Db | | | | |
 XX 1 ADWSWA 6
 XX
 XX RESULT 17
 XX ADA61849
 XX ID ADA61849 standard; peptide; 9 AA.
 XX
 XX AC ADA61849;
 XX
 XX DT 20-NOV-2003 (first entry)
 XX
 XX DE NFkB essential modulator (NEMO) binding peptide #49.
 XX
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX antiarthritic; osteoprotective; antibacterial; immunosuppressive;
 XX dermatological; neuroprotective; cytostatic; nootropic; virucide;
 XX gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 XX psoriasis; rheumatoid arthritis; osteoarthritis;
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 XX Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 XX necrosis factor kappa B essential modulator.
 XX
 XX OS Unidentified.
 XX
 XX US2003054999-A1.
 XX
 XX PD 20-MAR-2003.
 XX
 XX PF 02-MAY-2001; 2001US-00847946.
 XX
 XX PR 02-MAY-2000; 2000US-0201261P.
 XX
 XX (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.
 XX (FIND/) FINDEIS M A.
 XX (PHIL/) PHILLIPS K.
 XX (HANN/) HANNIG G.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 XX PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 XX PT cancer, comprises a membrane translocation domain and a NEMO binding
 XX PT sequence.

PT New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 PT
 PS Claim 6; Page 23; 37pp; English.
 PS
 XX The invention describes an anti-inflammatory compound comprising (I). The
 XX compound is useful for diagnosing or treating inflammatory disorders,
 XX such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 XX inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 XX systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 XX Alzheimer's disease or viral infection. This is the amino acid sequence
 XX of an anti-inflammatory peptide that binds to, and down-regulates,
 XX necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX
 XX Sequence 9 AA;
 XX
 XX Query Match 100.0%; Score 6; DB 6; Length 9;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 ADWSWA 6
 XX Db | | | | |
 XX 2 ADWSWA 7
 XX
 XX RESULT 18
 XX ADA61845
 XX ID ADA61845 standard; peptide; 9 AA.
 XX
 XX AC ADA61845;
 XX
 XX DT 20-NOV-2003 (first entry)
 XX
 XX DE NFkB essential modulator (NEMO) binding peptide #45.
 XX
 XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX antiarthritic; osteoprotective; antibacterial; immunosuppressive;
 XX dermatological; neuroprotective; cytostatic; nootropic; virucide;
 XX gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 XX psoriasis; rheumatoid arthritis; osteoarthritis;
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 XX Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 XX necrosis factor kappa B essential modulator.
 XX
 XX OS Unidentified.
 XX
 XX US2003054999-A1.
 XX
 XX PD 20-MAR-2003.
 XX
 XX PF 02-MAY-2001; 2001US-00847946.
 XX
 XX PR 02-MAY-2000; 2000US-0201261P.
 XX
 XX (MAYM/) MAY M J.
 XX (GHOS/) GHOSH S.
 XX (FIND/) FINDEIS M A.
 XX (PHIL/) PHILLIPS K.
 XX (HANN/) HANNIG G.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 XX PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 XX PT cancer, comprises a membrane translocation domain and a NEMO binding
 XX PT sequence.

PS Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The

CC compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADWSWA 6

Db 1 ADWSWA 6

RESULT 19

ADA61842

ID ADA61842 standard; peptide; 9 AA.

AC ADA61842;

XX 20-NOV-2003 (first entry)

XX NFkB essential modulator (NEMO) binding peptide #42.

XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;

KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;

KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

KW dermatological; neuroprotective; cytostatic; nootropic; virucide;

KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;

KW psoriasis; rheumatoid arthritis; osteoarthritis;

KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;

KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;

KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX (FIND/) FINDEIS M A.

XX (PHIL/) PHILLIPS K.

XX (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.

PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or

PT cancer, comprises a membrane translocation domain and a NEMO binding

PT sequence.

XX Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The

CC compound is useful for diagnosing or treating inflammatory disorders,

CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,

CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.

CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence

CC of an anti-inflammatory peptide that binds to, and down-regulates,

CC necrosis factor kappa B (NFkB) essential modulator (NEMO).

XX Sequence 9 AA;

Query Match 100.0%; Score 6; DB 6; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ADWSWA 6

Db 1 ADWSWA 6

RESULT 20

AAM48568

ID AAM48568 standard; peptide; 10 AA.

XX AAM48568;

XX 20-MAR-2002 (first entry)

XX Anti-inflammatory peptide SEQ ID NO 71.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYIA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain

PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB

PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AAM4828-AAM48645), comprising a membrane translocation domain (AAM48620-

CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid

CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The

CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,

CC antirheumatic, antiarthritic, osteopathic, antibacterial,

CC immunosuppressive, dermatological, neuroprotective, nootropic,

CC antiatherosclerotic, virucide and anti allergic activity. The compounds

CC act as selective inhibitors of cytokine-mediated NFkappaB activation by

CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding

CC domain that results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compounds are useful

Mon Jul 26 09:11:20 2004

act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of I kappa B kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent dephosphorylation of I kappa B. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 10 AA;
 Query Match 100.0%; Score 6; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 |||||
 Db 3 ADWSWA 8
 |||||

RESULT 22
 ADA61844
 ID ADA61844 standard; peptide; 10 AA.
 AC ADA61844;
 DT 20-NOV-2003 (first entry)
 XX NFKB essential modulator (NEMO) binding peptide #44.
 DE NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytostatic; neutropenic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis; autoimmune disease;
 KW inflammatory bowel disease; sepsis; vasculitis; cancer; osteoporosis;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.
 XX Unidentified.
 OS
 XX US2003054999-A1.
 PN
 XX 20-MAR-2003.
 PD
 XX 02-MAY-2001; 2001US-00847946.
 PF
 XX 02-MAY-2000; 2000US-0201261P.
 PR
 XX (MAYM/) MAY M J.
 PA (GHOS/) GHOSH S.
 PA (FIND/) FINDEIS M A.
 PA (PHIL/) PHILLIPS K.
 PA (HANN/) HANNIG G.
 XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 PI WPI; 2003-596541/56.
 DR
 XX New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.
 PT
 XX Claim 6; Page 23; 37pp; English.

for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis

Sequence 10 AA;
 Query Match 100.0%; Score 6; DB 5; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSWA 6
 |||||
 Db 2 ADWSWA 7
 |||||

RESULT 21
 AAM48571
 ID AAM48571 standard; peptide; 10 AA.
 AC AAM48571;
 DT 20-MAR-2002 (first entry)
 XX Anti-inflammatory peptide SEQ ID NO 74.
 DE Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropenic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiinflammatory; membrane translocation domain; NEMO binding domain; eczema;
 KW antiasthmatic; NFKB kinase beta; IKKbeta; cancer; psoriasis;
 KW cytokine; NFKB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX WO200183554-A2.
 FN
 XX 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001WO-US014346.
 XX
 XX 02-MAY-2000; 2000US-0201261P.
 XX
 XX 22-AUG-2000; 2000US-00643260.
 XX
 XX (PRAE-) PRAECIS PHARM INC.
 XX
 XX (UYVA) UNIV YALE.
 XX
 XX May MJ, Ghosh S, Findeis MA, Phillips K;
 XX
 XX WPI; 2002-121889/16.
 XX
 XX Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappaB activation, and for treating asthma, lung inflammation, psoriasis.
 PT
 XX Claim 6; Page 62; 88pp; English.
 PS
 XX The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, neutropenic, antiatherosclerotic, virucide and antiasthmatic activity. The compounds

CC The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
 Db 2 ADWSWA 7
 |||||

RESULT 23
 ADA61847
 ID ADA61847 standard; peptide; 10 AA.
 XX
 AC ADA61847;

20-NOV-2003 (first entry)

NFKB essential modulator (NEMO) binding peptide #47.

KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
 KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 KW psoriasis; rheumatoid arthritis; osteoarthritis;
 KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 KW necrosis factor kappa B essential modulator.

XX Unidentified.

XX US2003054999-A1.

XX 20-MAR-2003.

XX 02-MAY-2001; 2001US-00847946.

XX 02-MAY-2000; 2000US-0201261P.

XX (MAYM/) MAY M J.

XX (GHOS/) GHOSH S.

XX (FIND/) FINDEIS M A.

XX (PHIL/) PHILLIPS K.

XX (HANN/) HANNIG G.

XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;

XX WPI; 2003-596541/56.

XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.

PS Claim 6; Page 23; 37pp; English.

XX The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,

CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 6; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSWA 6
 Db 3 ADWSWA 8
 |||||

RESULT 24
 AAM48565
 ID AAM48565 standard; peptide; 11 AA.
 XX
 AC AAM48565;

20-MAR-2002 (first entry)

Anti-inflammatory peptide SEQ ID NO 68.

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014346.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation domain
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
 PT activation, and for treating asthma, lung inflammation, psoriasis.

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially
 CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
 CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
 CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
 CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,
 CC immunosuppressive, dermatological, neuroprotective, nootropic,
 CC antiatherosclerotic, virucide and antiallergic activity. The compounds
 CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
 CC domain that results in inhibition of IKKbeta kinase activation and
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory

CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX
XX Sequence 11 AA;
Query Match 100.0%; Score 6; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
Db 3 ADWSWA 8
RESULT 25
ADA61840
ID ADA61840 standard; peptide; 11 AA.
XX
AC ADA61840;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFkB essential modulator (NEMO) binding peptide #40.
XX
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antinflammatory; antiarthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
XX Unidentified.
XX
XX US2003054999-A1.
XX
XX
PD 20-MAR-2003.
XX
XX 02-MAY-2001; 2001US-00847946.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
PI
XX WPI; 2003-596541/56.
DR
XX New compound for diagnosing or treating inflammatory disorders, e.g.
FT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
PS Claim 6; Page 23; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC

CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 11 AA;
Query Match 100.0%; Score 6; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSWA 6
Db 3 ADWSWA 8
RESULT 26
ABB08727
ID ABB08727 standard; peptide; 6 AA.
XX
AC ABB08727;
XX
DT 14-JUN-2002 (first entry)
XX
DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 4.
XX
XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiaesthatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Wildtype Leu substituted by Ala"
FT
FT WO200183547-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US040654.
XX
XX 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
XX (UYA) UNIV YALE.
PA
XX May MJ, Ghosh S;
PI
XX WPI; 2002-179350/23.
DR
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain.
XX
XX Claim 23; Page 44; 82pp; English.
XX
XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprising contacting a cell with an anti-inflammatory compound (ABB08725-
CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
CC compound has acts through selective inhibition of cytokine-mediated NF-kB
CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO
CC binding domain. Blockage of IKKbeta kinase activation and subsequent results in
CC inhibition of IKKbeta kinase activation and subsequent results in
CC phosphorylation of IkappaB. The compound may also act (directly or
CC indirectly) by blocking the recruitment of leukocytes into sites of acute

CC and chronic inflammation, by down-regulating the expression of E-selectin
 CC on leukocytes or by blocking osteoclast differentiation. The compound is
 CC useful in treating NF-kB mediated conditions, where the condition is an
 CC inflammatory disorder, an autoimmune disease, transplant rejection,
 CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
 CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
 CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
 CC inflammatory bowel disease, chronic obstructive pulmonary disease,
 CC vasculitis and bursitis. The inflammatory disorder may also be
 CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic colitis, lupus
 CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta

XX Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ADWSW 5

Db 1 ADWSW 5

RESULT 27

ID ABB08728 standard; peptide; 6 AA.

XX ABB08728;

DT 14-JUN-2002 (first entry)

DE Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.

KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
 KW dermatological; antibacterial; antiulcer; mutant; antirheumatic;
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "Wildtype Leu substituted by Ala"

XX WO200183547-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US040654.

XX 02-MAY-2000; 2000US-0201261P.

XX 22-AUG-2000; 2000US-00643260.

XX

PA (UYA) UNIV YALE.

XX May M7, Ghosh S;

XX WPI; 2002-179350/23.

XX Modulating NF-kappaB induction in a cell, useful for treating e.g.
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
 PT cell with an anti-inflammatory compound comprising at least one NEMO
 PT binding domain.

XX Claim 23; Page 44; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
 CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-
 CC ABB08742) comprising at least one NEMO binding domain (ABB77313). The
 CC compound has acts through selective inhibition of cytokine-mediated NF-kB
 CC activation by blocking the interaction of NEMO with IKKbeta at the NEMO
 CC binding domain. Blockage of IKKbeta-NEMO interaction results in
 CC inhibition of IKKbeta kinase activation and subsequent decreased
 CC phosphorylation of IkappaB. The compound may also act (directly or
 CC indirectly) by blocking the recruitment of leukocytes into sites of acute
 CC and chronic inflammation, by down-regulating the expression of E-selectin
 CC on leukocytes or by blocking osteoclast differentiation. The compound is
 CC useful in treating NF-kB mediated conditions, where the condition is an
 CC inflammatory disorder, an autoimmune disease, transplant rejection,
 CC osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
 CC infection or ataxia telangiectasia. The inflammatory disorder is asthma,
 CC allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
 CC psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
 CC inflammatory bowel disease, chronic obstructive pulmonary disease,
 CC vasculitis and bursitis. The inflammatory disorder may also be
 CC dermatitis, eczema, psoriasis, osteoarthritis, psoriatic colitis, lupus
 CC and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral
 CC diseases include HIV and influenza. The compound may also be useful for
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,
 CC sunburn or aging. The compound may be used to replace corticosteroids in
 CC any application in which corticosteroids are used, including
 CC immunosuppression in transplants and cancer therapy. Also for identifying
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.
 CC The compound may be administered alone or in combination with other known
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO
 CC binding domain of IKKbeta

XX Sequence 6 AA;

Query Match 83.3%; Score 5; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWSWA 6

Db 2 DWSWA 6

RESULT 28

ID AAM48537 standard; peptide; 6 AA.

XX AAM48537;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 40.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiarteriosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NPKappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014346.
XX 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX (PRAE-) PRACIS PHARM INC.
PA (UYVA) UNIV YALE.
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation domain
fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
activation, and for treating asthma, lung inflammation, psoriasis.
XX Claim 6; Page 61; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX Sequence 6 AA;
SQ
Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DMSWA 6
Db 2 DMSWA 6
RESULT 29
AAM48548
ID AAM48548 standard; peptide; 6 AA.
XX AAM48548;
AC
XX
XX 20-MAR-2002 (first entry)
DT Anti-inflammatory peptide SEQ ID NO 51.
DE
XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW anti allergic; membrane translocation domain; NEMO binding domain; eczema;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW autoimmune disorder; multiple sclerosis; transplant rejection;
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX Synthetic.
XX WO200183554-A2.
XX 08-NOV-2001.
XX 02-MAY-2001; 2001WO-US014346.
XX 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX (PRAE-) PRACIS PHARM INC.
PA (UYVA) UNIV YALE.
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX Novel antiinflammatory compound comprising membrane translocation domain
fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
activation, and for treating asthma, lung inflammation, psoriasis.
XX Claim 6; Page 62; 88pp; English.
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC antirheumatic, antiarthritic, osteopathic, antibacterial,
CC immunosuppressive, dermatological, neuroprotective, nootropic,
CC antiatherosclerotic, virucide and antiallergic activity. The compounds
CC act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC domain that results in inhibition of IKKbeta kinase activation and
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC viral infections; and ataxia telangiectasia. The compounds are also
CC useful for treating pro-inflammatory responses such as allergies,
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC sunburn, aging and arthritis
XX Sequence 6 AA;
SQ
Query Match 83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ADWSW 5
Db 1 ADWSW 5
RESULT 30
AAM48559
ID AAM48559 standard; peptide; 6 AA.
XX AAM48559;
AC
XX 20-MAR-2002 (first entry)
DT

Mon Jul 26 09:11:20 2004

QY	2	DMSWA 6	
DB	2	DMSWA 6	
RESULT 33			
AAAM48510			
ID	AAAM48510	standard; peptide; 6 AA.	
XX	AAAM48510;		
AC	20-MAR-2002	(first entry)	
DT	NBD mutant peptide SEQ ID NO 5.		
XX			
DE	Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;		
XX	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;		
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;		
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;		
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;		
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;		
KW	autoimmune disorder; multiple sclerosis; transplant rejection;		
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;		
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.		
OS	Synthetic.		
XX	WO200183554-A2.		
PN	08-NOV-2001.		
PD	02-MAY-2001; 2001WO-US014346.		
PF	02-MAY-2000; 2000US-0201261P.		
XX	22-AUG-2000; 2000US-00643260.		
PR	(PRAE-) PRAECIS PHARM INC.		
XX	(UYVA) UNIV YALE.		
PA	May MJ, Ghosh S, Findeis MA, Phillips K;		
PI	WPI; 2002-121889/16.		
DR	Novel antiinflammatory compound comprising membrane translocation domain		
XX	fused to NEMO binding sequence, useful for blocking nuclear factor kappaB		
PT	activation, and for treating asthma, lung inflammation, psoriasis.		
PT	Example 6; Page 47; 88pp; English.		
XX	The invention relates to an antiinflammatory compound (especially		
CC	AAAM48628-AAAM48645), comprising a membrane translocation domain (AAAM48620-		
CC	AAAM48627 or AAAM48646-AAAM48651) which comprises from 6-15 amino acid		
CC	residues, fused to a NEMO binding sequence (AAAM48525-AAAM48619). The		
CC	antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,		
CC	antirheumatic, antiarthritic, osteopathic, antibacterial,		
CC	immunosuppressive, dermatological, neuroprotective, nootropic,		
CC	antiatherosclerotic, virucide and antiallergic activity. The compounds		
CC	act as selective inhibitors of cytokine-mediated NFkappaB activation by		
CC	blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding		
CC	domain that results in inhibition of IkappaB kinase activation and		
CC	subsequent decreased phosphorylation of IkappaB. The compounds are useful		
CC	for treating inflammatory disorders, e.g. asthma, lung inflammation or		
CC	cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory		
CC	bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as		
CC	lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;		
CC	transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;		
CC	viral infections; and ataxia telangiectasia. The compounds are also		
CC	useful for treating pro-inflammatory responses such as allergies,		
CC	urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,		
CC	sunburn, aging and arthritis		
XX	Sequence 6 AA;		
SQ	Query Match 83.3%; Score 5; DB 5; Length 6;		
	Best Local Similarity 100.0%; Pred. No. 1.4e+06;		
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

```
Query Match      83.3%; Score 5; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 1 ADMSW 5
|||||
1 ADMSW 5

RESULT 34
ABU08420
ID ABU08420 standard; peptide; 6 AA.
XX
AC ABU08420;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human NEMO binding site (NBD) mutant peptide #3.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic; cytostatic;
KW neutropic; neuroprotective; antiatherosclerotic; virucide; vasotropic;
KW antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-00847940.
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
PR 22-AUG-2000; 2000US-00643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
WPI; 2003-209142/20.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding domain,
PT useful for modulating NF-kappaB induction in a cell and for treating NF-
PT kappaB-mediated inflammation disorders e.g., asthma, psoriasis,
PT vasculitis.
XX
PS Claim 22; Page 17; 47pp; English.
XX
CC The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are found on
CC IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha)
CC proteins. The antiinflammatory compounds of the invention are useful for
CC modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where
CC the compounds are capable of blocking the interaction between one or more
CC IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound
CC further comprises at least one membrane translocation domain. The
CC compounds are useful for treating inflammatory disorders, autoimmune
CC diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis,
CC viral infections, Ataxia telangiectasia, and for transplantation
CC detection. The compounds of the invention block NF-kappaB induction by
CC IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432
CC represent human NBD mutant peptides
XX
SQ Sequence 6 AA;

Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5
DB 1 ADMSW 5
|||||
1 ADMSW 5

RESULT 35
ABU08421
ID ABU08421 standard; peptide; 6 AA.
XX
AC ABU08421;
XX
DT 12-JUN-2003 (first entry)
XX
DE Human NEMO binding site (NBD) mutant peptide #4.
XX
KW Human; antiinflammatory compound; NEMO binding domain; NBD; IKKbeta;
KW IkappaB kinase-beta; IkappaB kinase-alpha; IKKalpha; NF-kappaB;
KW nuclear factor-kappaB induction; inflammatory disorder;
KW autoimmune disease; osteoporosis; cancer; Alzheimer's disease;
KW atherosclerosis; viral infection; Ataxia telangiectasia;
KW transplantation detection; immunosuppressive; osteopathic; cytostatic;
KW neutropic; neuroprotective; antiatherosclerotic; virucide; vasotropic;
KW antirheumatic; antiarthritic; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US2002156000-A1.
XX
PD 24-OCT-2002.
XX
PF 02-MAY-2001; 2001US-00847940.
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
PR 22-AUG-2000; 2000US-00643260.
XX
PA (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
XX
PI May MJ, Ghosh S;
XX
WPI; 2003-209142/20.
XX
PT Novel antiinflammatory peptide compounds comprising NEMO binding domain,
PT useful for modulating NF-kappaB induction in a cell and for treating NF-
PT kappaB-mediated inflammation disorders e.g., asthma, psoriasis,
PT vasculitis.
XX
PS Claim 22; Page 17; 47pp; English.
XX
CC The present invention relates to antiinflammatory compounds comprising
CC NEMO binding domain (NBD) peptides. The NEMO binding domains are found on
CC IkappaB kinase-beta (IKKbeta) and IkappaB kinase-alpha (IKKalpha)
CC proteins. The antiinflammatory compounds of the invention are useful for
CC modulating nuclear factor-kappaB (NF-kappaB) induction in a cell, where
CC the compounds are capable of blocking the interaction between one or more
CC IKKs such as IKKalpha or IKKbeta, and NEMO. The antiinflammatory compound
CC further comprises at least one membrane translocation domain. The
CC compounds are useful for treating inflammatory disorders, autoimmune
CC diseases, osteoporosis, cancer, Alzheimer's disease, atherosclerosis,
CC viral infections, Ataxia telangiectasia, and for transplantation
CC detection. The compounds of the invention block NF-kappaB induction by
CC IKK but do not inhibit the basal activity of NF-kappaB. ABU08418-ABU08432
CC represent human NBD mutant peptides
XX
SQ Sequence 6 AA;

Query Match      83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

ADA61811
ADA61811 standard: peptide; 6 AA.

XX AC ADA61811;
 XX DT 20-NOV-2003 (first entry)
 XX DE NFkB essential modulator (NEMO) binding peptide #11.
 XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 XX KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
 XX KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 XX KW psoriasis; rheumatoid arthritis; osteoarthritis;
 XX KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 XX KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 XX KW necrosis factor kappa B essential modulator.
 XX OS Unidentified.
 XX PN US2003054999-A1.
 XX PD 20-MAR-2003.
 XX PF 02-MAY-2001; 2001US-00847946.
 XX PR 02-MAY-2000; 2000US-0201261P.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PA (FIND/) FINDEIS M A.
 XX PA (PHIL/) PHILLIPS K.
 XX PA (HANN/) HANNIG G.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX PT New compound for diagnosing or treating inflammatory disorders, e.g.
 XX PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 XX PT cancer, comprises a membrane translocation domain and a NEMO binding
 XX PT sequence.
 XX PS Claim 6; Page 23; 37pp; English.
 XX CC The invention describes an anti-inflammatory compound comprising (I). The
 XX CC compound is useful for diagnosing or treating inflammatory disorders,
 XX CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 XX CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 XX CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 XX CC Alzheimer's disease or viral infection. This is the amino acid sequence
 XX CC of an anti-inflammatory peptide that binds to, and down-regulates,
 XX CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX SQ Sequence 6 AA;
 XX Query Match 83.3%; Score 5; DB 6; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 DB 1 ADWSW 5
 RESULT 39
 ADA61813
 ID ADA61813 standard; peptide; 6 AA.
 XX AC ADA61813;
 XX DT 20-NOV-2003 (first entry)
 XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 XX KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
 XX KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 XX KW psoriasis; rheumatoid arthritis; osteoarthritis;
 XX KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 XX KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 XX KW necrosis factor kappa B essential modulator.

DE XX NFkB essential modulator (NEMO) binding peptide #13.
 XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
 XX KW dermatological; neuroprotective; cytostatic; nootropic; virucide;
 XX KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
 XX KW psoriasis; rheumatoid arthritis; osteoarthritis;
 XX KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
 XX KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
 XX KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
 XX KW necrosis factor kappa B essential modulator.
 XX OS Unidentified.
 XX PN US2003054999-A1.
 XX PD 20-MAR-2003.
 XX PF 02-MAY-2001; 2001US-00847946.
 XX PR 02-MAY-2000; 2000US-0201261P.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PA (FIND/) FINDEIS M A.
 XX PA (PHIL/) PHILLIPS K.
 XX PA (HANN/) HANNIG G.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX PT New compound for diagnosing or treating inflammatory disorders, e.g.
 XX PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 XX PT cancer, comprises a membrane translocation domain and a NEMO binding
 XX PT sequence.
 XX PS Claim 6; Page 23; 37pp; English.
 XX CC The invention describes an anti-inflammatory compound comprising (I). The
 XX CC compound is useful for diagnosing or treating inflammatory disorders,
 XX CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 XX CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 XX CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 XX CC Alzheimer's disease or viral infection. This is the amino acid sequence
 XX CC of an anti-inflammatory peptide that binds to, and down-regulates,
 XX CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX SQ Sequence 6 AA;
 XX Query Match 83.3%; Score 5; DB 6; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DWSWA 6
 DB 2 DWSWA 6
 RESULT 40
 ADA61835
 ID ADA61835 standard; peptide; 6 AA.
 XX AC ADA61835;
 XX DT 20-NOV-2003 (first entry)
 XX KW NFkB essential modulator (NEMO) binding peptide #35.
 XX KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
 XX KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
 XX KW antiarthritic; osteopathic; antibacterial; immunosuppressive;

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KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
XX Unidentified.
OS
XX
PN US2003054999-A1.
XX
PD 20-MAR-2003.
XX
XX
PF 02-MAY-2001; 2001US-00847946.
XX
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
XX
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Claim 6; Page 23; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of an anti-inflammatory peptide that binds to, and down-regulates,
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
XX Sequence 6 AA;
SQ
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSWA 6
Db |||||
2 DWSWA 6
RESULT 41
ADA61779
ID ADA61779 standard; peptide; 6 AA.
XX
XX ADA61779;
XX
XX 20-NOV-2003 (first entry)
XX
XX IKKbeta NEMO binding domain (NBD) mutant #4.
XX
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;

KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator; mutant; mutein.
XX
XX Synthetic.
OS
XX Homo sapiens.
PN US2003054999-A1.
XX
XX 20-MAR-2003.
XX
XX
PF 02-MAY-2001; 2001US-00847946.
XX
XX
PR 02-MAY-2000; 2000US-0201261P.
XX
XX (MAYM/) MAY M J.
PA (GHOS/) GHOSH S.
PA (FIND/) FINDEIS M A.
PA (PHIL/) PHILLIPS K.
PA (HANN/) HANNIG G.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX WPI; 2003-596541/56.
XX
XX New compound for diagnosing or treating inflammatory disorders, e.g.
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT cancer, comprises a membrane translocation domain and a NEMO binding
PT sequence.
XX
XX Example 4; Page 19; 37pp; English.
XX
XX The invention describes an anti-inflammatory compound comprising (I). The
CC compound is useful for diagnosing or treating inflammatory disorders,
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC Alzheimer's disease or viral infection. This is the amino acid sequence
CC of I kappa B kinase beta (IKKbeta) NEMO binding domain (NBD) mutant
CC used in to determine which residues in the NBD are important for binding
CC NEMO (necrosis factor kappa B essential modulator).
XX
XX Sequence 6 AA;
SQ
Query Match 83.3%; Score 5; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSWA 6
Db |||||
2 DWSWA 6
RESULT 42
ADA61824
ID ADA61824 standard; peptide; 6 AA.
XX
XX ADA61824;
XX
XX 20-NOV-2003 (first entry)
XX
XX NFkB essential modulator (NEMO) binding peptide #24.
XX
XX NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW anti-inflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytotstatic; nootropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX

OS Unidentified.
 XX PN US2003054999-A1.
 XX PD 20-MAR-2003.
 XX PF 02-MAY-2001; 2001US-00847946.
 XX PR 02-MAY-2000; 2000US-0201261P.
 XX PA (MAYM/) MAY M J.
 XX PA (GHOS/) GHOSH S.
 XX PA (FIND/) FINDEIS M A.
 XX PA (PHIL/) PHILLIPS K.
 XX PA (HANN/) HANNIG G.
 XX PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
 XX WPI; 2003-596541/56.
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 XX Claim 6; Page 23; 37pp; English.
 XX The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX Sequence 6 AA;
 SQ
 Query Match 83.3%; Score 5; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 DB 1 ADWSW 5
 RESULT 43
 AAM48552
 ID AAM48552 standard; peptide; 7 AA.
 XX AC AAM48552;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 55.
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antiarthritis; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS WO200183554-A2.
 XX PN 08-NOV-2001.
 XX PD
 XX PF
 XX PR
 XX PA
 XX PI
 XX WPI; 2003-596541/56.
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 XX Claim 6; Page 23; 37pp; English.
 XX The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX Sequence 6 AA;
 SQ
 Query Match 83.3%; Score 5; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 DB 1 ADWSW 5
 RESULT 43
 AAM48552
 ID AAM48552 standard; peptide; 7 AA.
 XX AC AAM48552;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 55.
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antiarthritis; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS WO200183554-A2.
 XX PN 08-NOV-2001.
 XX PD
 XX PF
 XX PR
 XX PA
 XX PI
 XX WPI; 2003-596541/56.
 XX New compound for diagnosing or treating inflammatory disorders, e.g.
 PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
 PT cancer, comprises a membrane translocation domain and a NEMO binding
 PT sequence.
 XX Claim 6; Page 23; 37pp; English.
 XX The invention describes an anti-inflammatory compound comprising (I). The
 CC compound is useful for diagnosing or treating inflammatory disorders,
 CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
 CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
 CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
 CC Alzheimer's disease or viral infection. This is the amino acid sequence
 CC of an anti-inflammatory peptide that binds to, and down-regulates,
 CC necrosis factor kappa B (NFkB) essential modulator (NEMO).
 XX Sequence 6 AA;
 SQ
 Query Match 83.3%; Score 5; DB 5; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ADWSW 5
 DB 1 ADWSW 5
 RESULT 44
 AAM48563
 ID AAM48563 standard; peptide; 7 AA.
 XX AC AAM48563;
 XX DT 20-MAR-2002 (first entry)
 XX DE Anti-inflammatory peptide SEQ ID NO 66.
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;
 KW antiarthritis; osteopathic; antibacterial; virucide;
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
 KW autoimmune disorder; multiple sclerosis; transplant rejection;
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.
 XX Synthetic.
 OS
 XX
 XX

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Alzheimer's disease; viral infection; NF-kappa B essential modulator;
necrosis factor kappa B essential modulator.

Unidentified.
US2003054999-A1.
20-MAR-2003.
02-MAY-2001; 2001US-00847946.
02-MAY-2000; 2000US-0201261P.
(MAYN/) MAY M J.
(GROS/) GHOSH S.
(FINDS/) FINDELS M A.
(PHIL/) PHILLIPS K.
(HANN/) HANNIG G.
May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
WPI; 2003-596541/56.
New compound for diagnosing or treating inflammatory disorders, e.g. asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or cancer, comprises a membrane translocation domain and a NEMO binding sequence.
Claim 6; Page 23; 37pp; English.
The invention describes an anti-inflammatory compound comprising (i). The compound is useful for diagnosing or treating inflammatory disorders, such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis, Alzheimer's disease or viral infection. This is the amino acid sequence of an anti-inflammatory peptide that binds to, and down-regulates, necrosis factor kappa B (NFkB) essential modulator (NEMO).
Sequence 7 AA;
Query Match 83.3%; Score 5; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ADWSW 5
Db 1 ADWSW 5
|||||
RESULT 46
ADA61839
ID ADA61839 standard; peptide; 7 AA.
XX
AC ADA61839;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFKB essential modulator (NEMO) binding peptide #39.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutrotropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;
KW necrosis factor kappa B essential modulator.
XX
OS Unidentified.
XX

WO200183554-A2.
08-NOV-2001.
02-MAY-2001; 2001WO-US014346.
02-MAY-2000; 2000US-0201261P.
22-AUG-2000; 2000US-00843260.
(PRAE-) PRAECIS PHARM INC.
(UYVA) UNIV YALE.
May MJ, Ghosh S, Findeis MA, Phillips K;
WPI; 2002-121889/16.
Novel antiinflammatory compound comprising membrane translocation domain fused to NEMO binding sequence, useful for blocking nuclear factor kappab activation, and for treating asthma, lung inflammation, psoriasis.
Claim 6; Page 62; 89pp; English.
The invention relates to an antiinflammatory compound (especially AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, antineoplastic, immunosuppressive, dermatological, neuroprotective, neutrotropic, antithrombotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappab activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis
Sequence 7 AA;
Query Match 83.3%; Score 5; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DWSWA 6
Db 2 DWSWA 6
|||||
RESULT 45
ADA61828
ID ADA61828 standard; peptide; 7 AA.
XX
AC ADA61828;
XX
DT 20-NOV-2003 (first entry)
XX
DE NFKB essential modulator (NEMO) binding peptide #28.
XX
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;
KW antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antibacterial; immunosuppressive;
KW dermatological; neuroprotective; cytostatic; neutrotropic; virucide;
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;
KW psoriasis; rheumatoid arthritis; osteoarthritis;
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;
KW


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PN  US2003054999-A1.
XX
PD  20-MAR-2003.
XX
XX  02-MAY-2001; 2001US-00847946.
XX
XX  02-MAY-2000; 2000US-0201261P.
XX
XX  (MAYM/) MAY M J.
PA  (GHOS/) GHOSH S.
PA  (FIND/) FINDEIS M A.
PA  (PHIL/) PHILLIPS K.
PA  (HANN/) HANNIG G.
XX
PI  May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;
XX
XX  WPI; 2003-596541/56.
XX
XX  New compound for diagnosing or treating inflammatory disorders, e.g.
PT  asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or
PT  cancer, comprises a membrane translocation domain and a NEMO binding
PT  sequence.
XX
XX  Claim 6; Page 23; 37pp; English.
XX
XX  The invention describes an anti-inflammatory compound comprising (I). The
CC  compound is useful for diagnosing or treating inflammatory disorders,
CC  such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,
CC  inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.
CC  systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,
CC  Alzheimer's disease or viral infection. This is the amino acid sequence
CC  of an anti-inflammatory peptide that binds to, and down-regulates,
CC  necrosis factor kappa B (NFkB) essential modulator (NEMO).
XX
SQ  Sequence 7 AA;
    Query Match      83.3%; Score 5; DB 6; Length 7;
    Best Local Similarity 100.0%; Pred. No. 1.4e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 DWSWA 6
    |||||
DB  2 DWSWA 6

RESULT 47
AAM48556
ID  AAM48556 standard; peptide; 8 AA.
XX
XX  AAM48556;
AC
XX
XX  20-MAR-2002 (first entry)
DT
XX
XX  Anti-inflammatory peptide SEQ ID NO 59.
DE
XX
XX  Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW  antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW  immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW  anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW  cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW  rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW  autoimmune disorder; multiple sclerosis; transplant rejection;
KW  osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW  ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX  Synthetic.
OS
XX  WO200183554-A2.
XX
XX  08-NOV-2001.
XX
XX  02-MAY-2001; 2001WO-US014346.
XX

PR  02-MAY-2000; 2000US-0201261P.
XX
XX  22-AUG-2000; 2000US-00643260.
XX
XX  (PRAE-) PRAECIS PHARM INC.
PA  (UYUA ) UNIV YALE.
XX
XX  May MJ, Ghosh S, Findeis MA, Phillips K;
PI  WPI; 2002-121889/16.
XX
XX  Novel antiinflammatory compound comprising membrane translocation domain
PT  fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT  activation, and for treating asthma, lung inflammation, psoriasis.
XX
XX  Claim 6; Page 62; 88pp; English.
XX
XX  The invention relates to an antiinflammatory compound (especially
CC  AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC  AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC  residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC  antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC  antirheumatic, antiarthritic, osteopathic, antibacterial,
CC  immunosuppressive, dermatological, neuroprotective, nootropic,
CC  antiatherosclerotic, virucide and anti-allergic activity. The compounds
CC  act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC  blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC  domain that results in inhibition of IKKbeta kinase activation and
CC  subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC  for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC  cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC  bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC  lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC  transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC  viral infections; and ataxia telangiectasia. The compounds are also
CC  useful for treating pro-inflammatory responses such as allergies,
CC  urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC  sunburn, aging and arthritis
XX
SQ  Sequence 8 AA;
    Query Match      83.3%; Score 5; DB 5; Length 8;
    Best Local Similarity 100.0%; Pred. No. 1.4e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 DWSWA 6
    |||||
DB  4 DWSWA 8

RESULT 48
AAM48545
ID  AAM48545 standard; peptide; 8 AA.
XX
XX  AAM48545;
AC
XX
XX  20-MAR-2002 (first entry)
DT
XX
XX  Anti-inflammatory peptide SEQ ID NO 48.
DE
XX
XX  Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW  antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW  immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW  anti-allergic; membrane translocation domain; NEMO binding domain; eczema;
KW  cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
KW  rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW  autoimmune disorder; multiple sclerosis; transplant rejection;
KW  osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW  ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX  Synthetic.
OS
XX  WO200183554-A2.
XX
XX  08-NOV-2001.
XX
XX  02-MAY-2001; 2001WO-US014346.
XX

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PS 08-NOV-2001.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
XX
XX 02-MAY-2000; 2000US-0201261P.
XX
XX 22-AUG-2000; 2000US-00643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX (UYVA ) UNIV YALE.
XX
XX May MJ, Ghosh S, Findeis MA, Phillips K;
XX WPI; 2002-121889/16.
XX
XX Novel antiinflammatory compound comprising membrane translocation domain
XX fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
XX activation, and for treating asthma, lung inflammation, psoriasis.
XX
XX Claim 6; Page 62; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
XX AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
XX AAM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
XX residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
XX antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
XX antirheumatic, antiarthritic, osteopathic, antibacterial,
XX immunosuppressive, dermatological, neuroprotective, nootropic,
XX antithrombotic, virucide and antiallergic activity. The compounds
XX act as selective inhibitors of cytokine-mediated NFkappaB activation by
XX blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
XX domain that results in inhibition of IKKbeta kinase activation and
XX subsequent decreased phosphorylation of IkappaB. The compounds are useful
XX for treating inflammatory disorders, e.g. asthma, lung inflammation or
XX cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
XX bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as
XX lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
XX transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
XX viral infections; and ataxia telangiectasia. The compounds are also
XX useful for treating pro-inflammatory responses such as allergies,
XX urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
XX sunburn, aging and arthritis
XX
XX Sequence 8 AA;
XX
Query Match 83.3%; Score 5; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADWSW 5
Db 3 ADWSW 7
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3 ADWSW 7

RESULT 49
AAM48564
ID AAM48564 standard; peptide; 8 AA.
XX
XX AAM48564;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 67.
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antithrombotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX

OS Synthetic.
XX
XX WO200183554-A2.
XX
XX 08-NOV-2001.
XX
XX 02-MAY-2001; 2001WO-US014346.
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XX 02-MAY-2000; 2000US-0201261P.
XX
XX 22-AUG-2000; 2000US-00643260.
XX
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XX transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
XX viral infections; and ataxia telangiectasia. The compounds are also
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XX urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
XX sunburn, aging and arthritis
XX
XX Sequence 8 AA;
XX
Query Match 83.3%; Score 5; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSWA 6
Db 2 DWSWA 6
|||||
2 DWSWA 6

RESULT 50
AAM48553
ID AAM48553 standard; peptide; 8 AA.
XX
XX AAM48553;
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 56.
XX
XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antithrombotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX

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